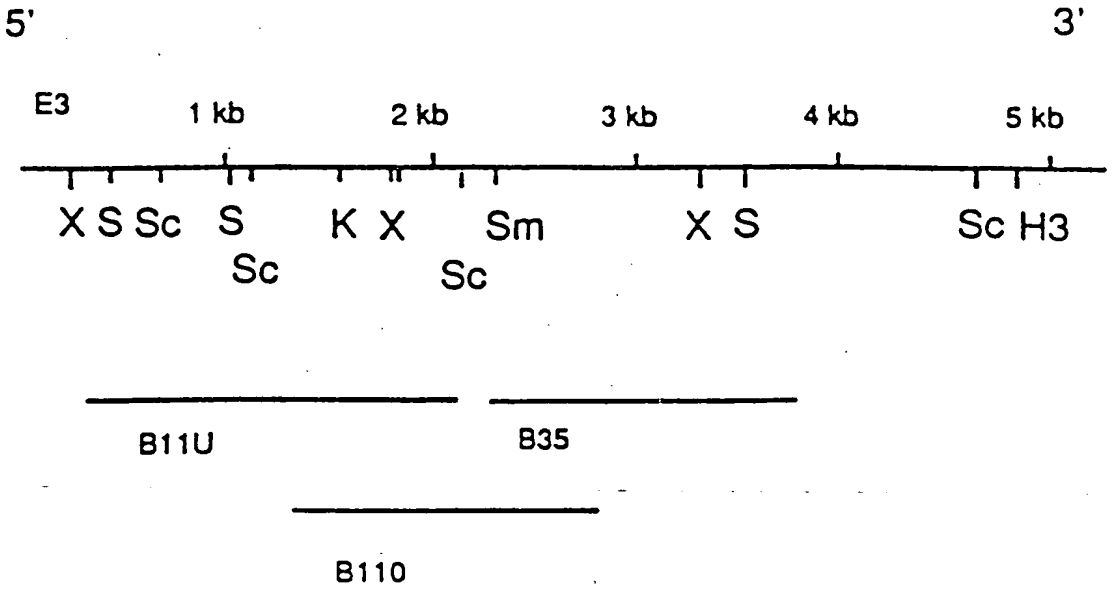
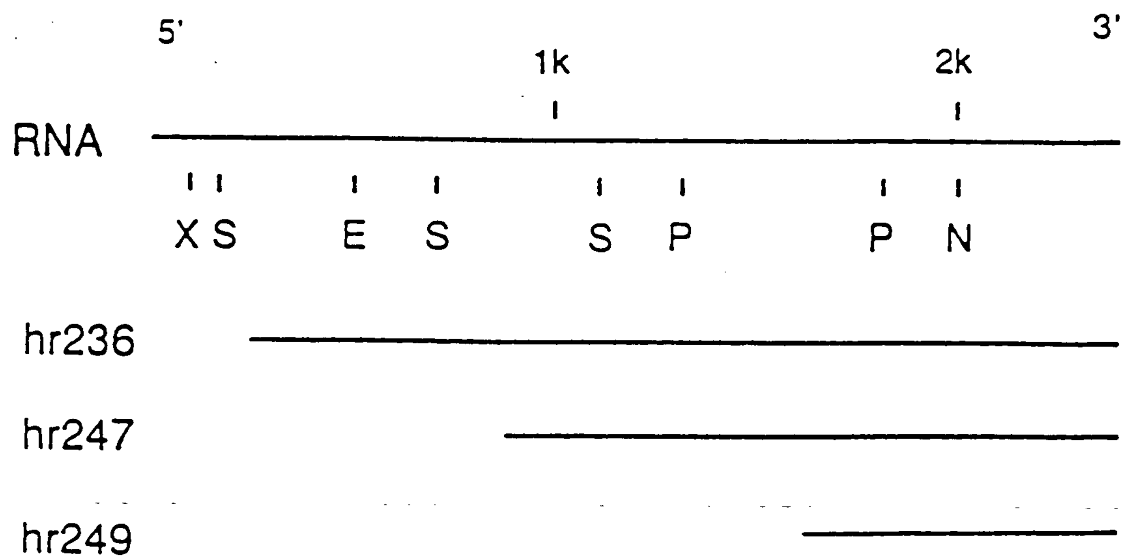
Map of HaSV RNA 1 clones



H3=Hind3, K=Kpn1, Sc=Sac1, S=Sal1, Sm=Sma1, X=Xho1

FIG. 1a.

Map of HaSV RNA 2 clones



E=EcoR1, N=Not1, P=Pst1, S=Sal1. X=Xho1

FIG. 1b

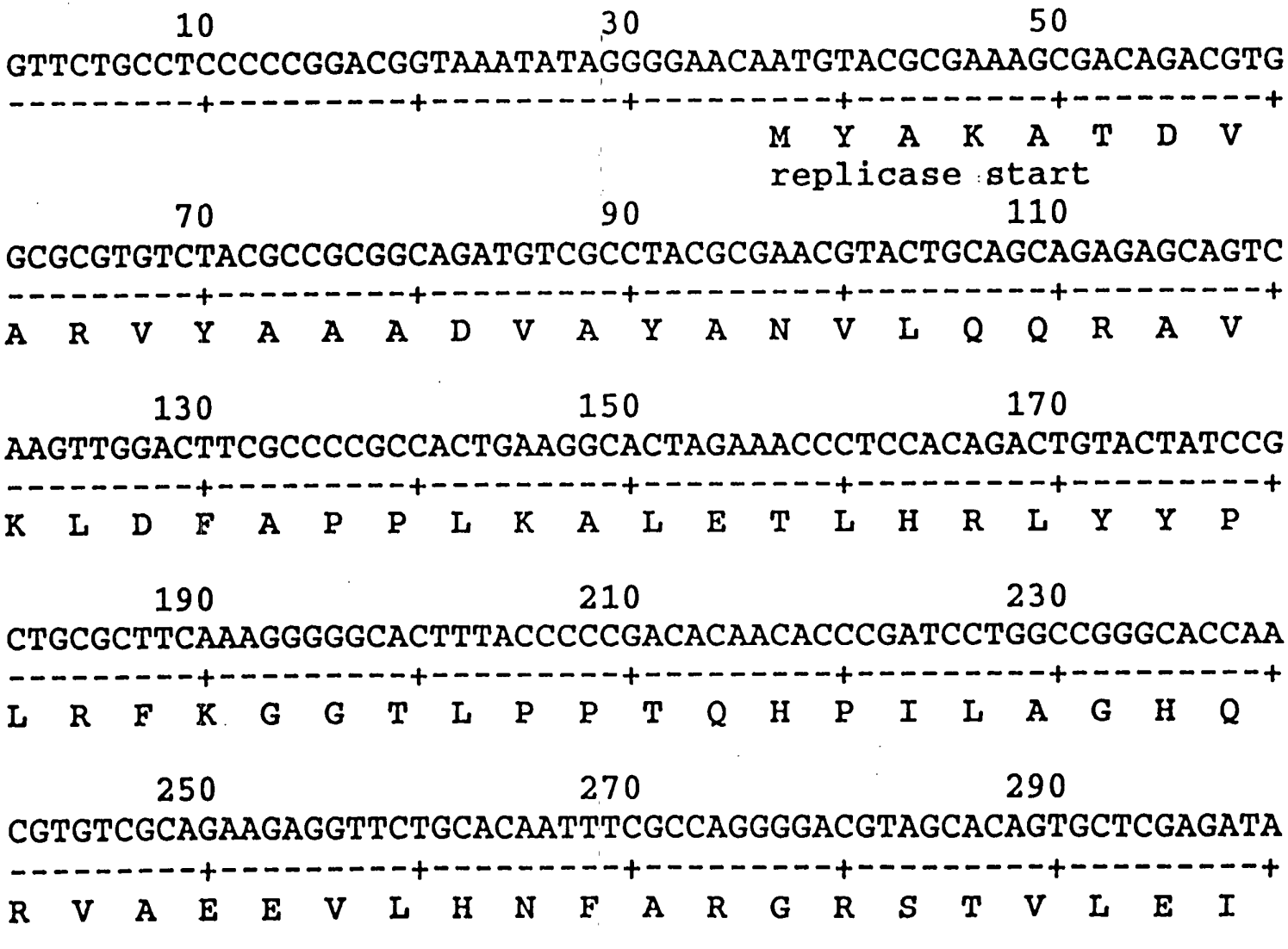

10
30
50
GTTCTGCCTCCCCCGGACGGTAAATATAGGGGAACAATGTACGCGAAAGCGACAGACGTG
M Y A K A T D V
replicase start
70
90
110
GCGCGTGTCTACGCCGCGGCAGATGTCGCCTACGCGAACGTACTGCAGCAGAGAGCAGTC
A R V Y A A A D V A Y A N V L Q Q R A V
130
150
170
AAGTTGGACTTCGCCCCGCCACTGAAGGCACTAGAAACCCTCCACAGACTGTACTATCCG
K L D F A P P L K A L E T L H R L Y Y P
190
210
230
CTGCGCTTCAAAGGGGGCACTTTACCCCCGACACAACACCCGATCCTGGCCGGGCACCAA
L R F K G G T L P P T Q H P I L A G H Q
250
270
290
CGTGTCGCAGAAGAGGTTCTGCACAATTTCGCCAGGGGACGTAGCACAGTGCTCGAGATA
R V A E E V L H N F A R G R S T V L E I

FIG. 2.1.

```
          310                           330                           350
GGGCCGTCTCTGCACAGCGCACTTAAGCTACATGGGGCACCGAACGCCCCCGTCGCAGAC
---------+---------+---------+---------+---------+---------+
G  P  S  L  H  S  A  L  K  L  H  G  A  P  N  A  P  V  A  D

          370                           390                           410
TATCACGGGTGCACCAAGTACGGCACCCGCGACGGCTCGCGACACATTACGGCCTTAGAG
---------+---------+---------+---------+---------+---------+
Y  H  G  C  T  K  Y  G  T  R  D  G  S  R  H  I  T  A  L  E

          430                           450                           470
TCTAGATCCGTCGCCACAGGCCGGCCCGAGTTCAAGGCCGACGCCTCACTGCTCGCCAAC
---------+---------+---------+---------+---------+---------+
S  R  S  V  A  T  G  R  P  E  F  K  A  D  A  S  L  L  A  N

          490                           510                           530
GGCATTGCCTCCCGCACCTTCTGCGTCGACGGAGTCGGCTCTTGCGCGTTCAAATCGCGC
---------+---------+---------+---------+---------+---------+
G  I  A  S  R  T  F  C  V  D  G  V  G  S  C  A  F  K  S  R

          550                           570                           590
GTTGGAATTGCCAATCACTCCCTCTATGACGTGACCCTAGAGGAGCTGGCCAATGCGTTT
---------+---------+---------+---------+---------+---------+
V  G  I  A  N  H  S  L  Y  D  V  T  L  E  E  L  A  N  A  F
```

FIG. 2.2

```
        610                 630                 650
GAGAACCACGGACTTCACATGGTCCGCGCGTTCATGCACATGCCAGAAGAGCTGCTCTAC
---------+---------+---------+---------+---------+---------+
E  N  H  G  L  H  M  V  R  A  F  M  H  M  P  E  E  L  L  Y

        670                 690                 710
ATGGACAACGTGGTTAATGCCGAGCTCGGCTACCGCTTCCACGTTATTGAAGAGCCTATG
---------+---------+---------+---------+---------+---------+
M  D  N  V  V  N  A  E  L  G  Y  R  F  H  V  I  E  E  P  M

        730                 750                 770
GCTGTGAAGGACTGCGCATTCCAGGGGGGGGACCTCCGTCTCCACTTCCCTGAGTTGGAC
---------+---------+---------+---------+---------+---------+
A  V  K  D  C  A  F  Q  G  G  D  L  R  L  H  F  P  E  L  D

        790                 810                 830
TTCATCAACGAGAGCCAAGAGCGGCGCATCGAGAGGCTGGCCGCCCGCGGCTCCTACTCC
---------+---------+---------+---------+---------+---------+
F  I  N  E  S  Q  E  R  R  I  E  R  L  A  A  R  G  S  Y  S

        850                 870                 890
AGACGCGCCGTCATTTTCTCCGGCGACGACGACTGGGGTGATGCGTACTTACACGACTTC
---------+---------+---------+---------+---------+---------+
R  R  A  V  I  F  S  G  D  D  D  W  G  D  A  Y  L  H  D  F
```

FIG. 23

```
       910                 930                 950
CACACATGGCTCGCCTACCTACTGGTGAGGAACTACCCCACTCCGTTTGGTTTCTCACTC
---------+---------+---------+---------+---------+---------+
H  T  W  L  A  Y  L  L  V  R  N  Y  P  T  P  F  G  F  S  L

       970                 990                1010
CATATAGAAGTCCAGAGGCGCCACGGCTCCAGCATTGAGCTGCGCATCACTCGCGCGCCA
---------+---------+---------+---------+---------+---------+
H  I  E  V  Q  R  R  H  G  S  S  I  E  L  R  I  T  R  A  P

      1030                1050                1070
CCTGGAGACCGCATGCTGGCCGTCGTCCCAAGGACGTCCCAAGGCCTCTGCAGAATCCCA
---------+---------+---------+---------+---------+---------+
P  G  D  R  M  L  A  V  V  P  R  T  S  Q  G  L  C  R  I  P

      1090                1110                1130
AACATCTTTTATTACGCCGACGCGTCGGGCACTGAGCATAAGACCATCCTTACGTCACAG
---------+---------+---------+---------+---------+---------+
N  I  F  Y  Y  A  D  A  S  G  T  E  H  K  T  I  L  T  S  Q

      1150                1170                1190
CACAAAGTCAACATGCTGCTCAATTTTATGCAAACGCGTCCTGAGAAGGAACTAGTCGAC
---------+---------+---------+---------+---------+---------+
H  K  V  N  M  L  L  N  F  M  Q  T  R  P  E  K  E  L  V  D
```

FIG. 2·4

```
      1210                 1230                 1250
ATGACCGTCTTGATGTCGTTCGCGCGCGCTAGGCTGCGCGCGATCGTGGTCGCCTCAGAA
---------+---------+---------+---------+---------+---------+---------+
M  T  V  L  M  S  F  A  R  A  R  L  R  A  I  V  V  A  S  E

      1270                 1290                 1310
GTCACCGAGAGCTCCTGGAACATCTCACCGGCTGACCTGGTCCGCACTGTCGTGTCTCTT
---------+---------+---------+---------+---------+---------+---------+
V  T  E  S  S  W  N  I  S  P  A  D  L  V  R  T  V  V  S  L

      1330                 1350                 1370
TACGTCCTCCACATCATCGAGCGCCGAAGGGCTGCGGTCGCTGTCAAGACCGCCAAGGAC
---------+---------+---------+---------+---------+---------+---------+
Y  V  L  H  I  I  E  R  R  R  A  A  V  A  V  K  T  A  K  D

      1390                 1410                 1430
GACGTCTTTGGAGAGACTTCGTTCTGGGAGAGTCTCAAGCACGTCTTGGGCTCCTGTTGC
---------+---------+---------+---------+---------+---------+---------+
D  V  F  G  E  T  S  F  W  E  S  L  K  H  V  L  G  S  C  C

      1450                 1470                 1490
GGTCTGCGCAACCTCAAAGGCACCGACGTCGTCTTTACTAAGCGCGTCGTCGATAAGTAC
---------+---------+---------+---------+---------+---------+---------+
G  L  R  N  L  K  G  T  D  V  V  F  T  K  R  V  V  D  K  Y
```

FIG. 2.5

```
        1510                1530                1550
CGAGTCCACTCGCTCGGAGACATAATCTGCGACGTCCGCCTGTCCCCTGAACAGGTCGGC
---------+---------+---------+---------+---------+---------+
R  V  H  S  L  G  D  I  I  C  D  V  R  L  S  P  E  Q  V  G

        1570                1590                1610
TTCCTGCCGTCCCGCGTACCACCTGCCCGCGTCTTTCACGACAGGGAAGAGCTTGAGGTC
---------+---------+---------+---------+---------+---------+
F  L  P  S  R  V  P  P  A  R  V  F  H  D  R  E  E  L  E  V

        1630                1650                1670
CTTCGCGAAGCTGGCTGCTACAACGAACGTCCGGTACCTTCCACTCCTCCTGTGGAGGAG
---------+---------+---------+---------+---------+---------+
L  R  E  A  G  C  Y  N  E  R  P  V  P  S  T  P  P  V  E  E

        1690                1710                1730
CCCCAAGGTTTCGACGCCGACTTGTGGCACGCGACCGCGGCCTCACTCCCCGAGTACCGC
---------+---------+---------+---------+---------+---------+
P  Q  G  F  D  A  D  L  W  H  A  T  A  A  S  L  P  E  Y  R

        1750                1770                1790
GCCACCTTGCAGGCAGGTCTCAACACCGACGTCAAGCAGCTCAAGATCACCCTCGAGAAC
---------+---------+---------+---------+---------+---------+
A  T  L  Q  A  G  L  N  T  D  V  K  Q  L  K  I  T  L  E  N
```

FIG. 2.6

```
      1810                  1830                  1850
GCCCTCAAGACCATCGACGGGCTCACCCTCTCCCCAGTCAGAGGCCTCGAGATGTACGAG
---------+---------+---------+---------+---------+---------+
A  L  K  T  I  D  G  L  T  L  S  P  V  R  G  L  E  M  Y  E

      1870                  1890                  1910
GGCCCGCCAGGCAGCGGCAAGACGGGCACCCTCATCGCCGCCCTTGAGGCCGCGGGCGGT
---------+---------+---------+---------+---------+---------+
G  P  P  G  S  G  K  T  G  T  L  I  A  A  L  E  A  A  G  G

      1930                  1950                  1970
AAAGCACTTTACGTGGCACCCACCAGAGAACTGAGAGAGGCTATGGACCGGCGGATCAAA
---------+---------+---------+---------+---------+---------+
K  A  L  Y  V  A  P  T  R  E  L  R  E  A  M  D  R  R  I  K

      1990                  2010                  2030
CCGCCGTCCGCCTCGGCTACGCAACATGTCGCCCTTGCGATTCTCCGTCGTGCCACCGCC
---------+---------+---------+---------+---------+---------+
P  P  S  A  S  A  T  Q  H  V  A  L  A  I  L  R  R  A  T  A

      2050                  2070                  2090
GAGGGCGCCCCTTTCGCTACCGTGGTTATCGACGAGTGCTTCATGTTCCCGCTCGTGTAC
---------+---------+---------+---------+---------+---------+
E  G  A  P  F  A  T  V  V  I  D  E  C  F  M  F  P  L  V  Y
```

FIG. 2-1

```
        2110                2130                2150
GTCGCGATCGTGCACGCCTTGTCCCCGAGCTCACGAATAGTCCTTGTAGGGGACGTCCAC
---------+---------+---------+---------+---------+---------+
V  A  I  V  H  A  L  S  P  S  S  R  I  V  L  V  G  D  V  H

        2170                2190                2210
CAAATCGGGTTTATAGACTTCCAAGGCACAAGCGCGAACATGCCGCTCGTTCGCGACGTC
---------+---------+---------+---------+---------+---------+
Q  I  G  F  I  D  F  Q  G  T  S  A  N  M  P  L  V  R  D  V

        2230                2250                2270
GTTAAGCAGTGCCGTCGGCGCACTTTCAACCAAACCAAGCGCTGTCCGGCCGACGTCGTT
---------+---------+---------+---------+---------+---------+
V  K  Q  C  R  R  R  T  F  N  Q  T  K  R  C  P  A  D  V  V

        2290                2310                2330
GCCACCACGTTTTTCCAGAGCTTGTACCCCGGGTGCACAACCACCTCAGGGTGCGTCGCA
---------+---------+---------+---------+---------+---------+
A  T  T  F  F  Q  S  L  Y  P  G  C  T  T  T  S  G  C  V  A

        2350                2370                2390
TCCATCAGCCACGTCGCCCCAGACTACCGCAACAGCCAGGCGCAAACGCTCTGCTTCACG
---------+---------+---------+---------+---------+---------+
S  I  S  H  V  A  P  D  Y  R  N  S  Q  A  Q  T  L  C  F  T
```

FIG. 2.8

```
      2410                2430                2450
CAGGAGGAAAAGTCGCGCCACGGGGCTGAGGGCGCGATGACTGTGCACGAAGCGCAGGGA
---------+---------+---------+---------+---------+---------+
Q  E  E  K  S  R  H  G  A  E  G  A  M  T  V  H  E  A  Q  G

      2470                2490                2510
CGCACTTTTGCGTCTGTCATTCTGCATTACAACGGCTCCACAGCAGAGCAGAAGCTCCTC
---------+---------+---------+---------+---------+---------+
R  T  F  A  S  V  I  L  H  Y  N  G  S  T  A  E  Q  K  L  L

      2530                2550                2570
GCTGAGAAGTCGCACCTTCTAGTCGGCATCACGCGCCACACCAACCACCTGTACATCCGC
---------+---------+---------+---------+---------+---------+
A  E  K  S  H  L  L  V  G  I  T  R  H  T  N  H  L  Y  I  R

      2590                2610                2630
GACCCGACAGGTGACATTGAGAGACAACTCAACCATAGCGCGAAAGCCGAGGTGTTTACA
---------+---------+---------+---------+---------+---------+
D  P  T  G  D  I  E  R  Q  L  N  H  S  A  K  A  E  V  F  T

      2650                2670                2690
GACATCCCTGCACCCCTGGAGATCACGACTGTCAAACCGAGTGAAGAGGTGCAGCGCAAC
---------+---------+---------+---------+---------+---------+
D  I  P  A  P  L  E  I  T  T  V  K  P  S  E  E  V  Q  R  N
```

FIG. 2-9

```
      2710                2730                2750
GAAGTGATGGCAACGATACCCCCGCAGAGTGCCACGCCGCACGGAGCAATCCATCTGCTC
---------+---------+---------+---------+---------+---------+
E  V  M  A  T  I  P  P  Q  S  A  T  P  H  G  A  I  H  L  L

      2770                2790                2810
CGCAAGAACTTCGGGGACCAACCCGACTGTGGCTGTGTCGCTTTGGCGAAGACCGGCTAC
---------+---------+---------+---------+---------+---------+
R  K  N  F  G  D  Q  P  D  C  G  C  V  A  L  A  K  T  G  Y

      2830                2850                2870
GAGGTGTTTGGCGGTCGTGCCAAAATCAACGTAGAGCTTGCCGAACCCGACGCGACCCCG
---------+---------+---------+---------+---------+---------+
E  V  F  G  G  R  A  K  I  N  V  E  L  A  E  P  D  A  T  P

      2890                2910                2930
AAGCCGCATAGGGCGTTCCAGGAAGGGGTACAGTGGGTCAAGGTCACCAACGCGTCTAAC
---------+---------+---------+---------+---------+---------+
K  P  H  R  A  F  Q  E  G  V  Q  W  V  K  V  T  N  A  S  N

      2950                2970                2990
AAACACCAGGCGCTCCAGACGCTGTTGTCCCGCTACACCAAGCGAAGCGCTGACCTGCCG
---------+---------+---------+---------+---------+---------+
K  H  Q  A  L  Q  T  L  L  S  R  Y  T  K  R  S  A  D  L  P
```

FIG. 2·10

```
      3010                  3030                  3050
CTACACGAAGCTAAGGAGGACGTCAAACGCATGCTAAACTCGCTTGACCGACATTGGGAC
---------+---------+---------+---------+---------+---------+
L  H  E  A  K  E  D  V  K  R  M  L  N  S  L  D  R  H  W  D

      3070                  3090                  3110
TGGACTGTCACTGAAGACGCCCGTGACCGAGCTGTCTTCGAGACCCAGCTCAAGTTCACC
---------+---------+---------+---------+---------+---------+
W  T  V  T  E  D  A  R  D  R  A  V  F  E  T  Q  L  K  F  T

      3130                  3150                  3170
CAACGCGGCGGCACCGTCGAAGACCTGCTGGAGCCAGACGACCCCTACATCCGTGACATA
---------+---------+---------+---------+---------+---------+
Q  R  G  G  T  V  E  D  L  L  E  P  D  D  P  Y  I  R  D  I

      3190                  3210                  3230
GACTTCCTTATGAAGACTCAGCAGAAAGTGTCGCCCAAGCCGATCAATACGGGCAAGGTC
---------+---------+---------+---------+---------+---------+
D  F  L  M  K  T  Q  Q  K  V  S  P  K  P  I  N  T  G  K  V

      3250                  3270                  3290
GGGCAGGGGATCGCCGCTCACTCAAAGTCTCTCAACTTCGTCCTCGCCGCTTGGATACGC
---------+---------+---------+---------+---------+---------+
G  Q  G  I  A  A  H  S  K  S  L  N  F  V  L  A  A  W  I  R
```

FIG. 2-11

```
        3310                3330                3350
ATACTCGAGGAGATACTCCGTACCGGGAGCCGCACGGTCCGGTACAGCAACGGTCTCCCC
---------+---------+---------+---------+---------+---------+
I  L  E  E  I  L  R  T  G  S  R  T  V  R  Y  S  N  G  L  P

        3370                3390                3410
GACGAAGAAGAGGCCATGCTGCTCGAAGCGAAGATCAATCAAGTCCCACACGCCACGTTC
---------+---------+---------+---------+---------+---------+
D  E  E  E  A  M  L  L  E  A  K  I  N  Q  V  P  H  A  T  F

        3430                3450                3470
GTCTCGGCGGACTGGACCGAGTTTGACACCGCCCACAATAACACGAGTGAGCTGCTCTTC
---------+---------+---------+---------+---------+---------+
V  S  A  D  W  T  E  F  D  T  A  H  N  N  T  S  E  L  L  F

        3490                3510                3530
GCCGCCCTTTTAGAGCGCATCGGCACGCCTGCAGCTGCCGTTAATCTATTCAGAGAACGG
---------+---------+---------+---------+---------+---------+
A  A  L  L  E  R  I  G  T  P  A  A  A  V  N  L  F  R  E  R

        3550                3570                3590
TGTGGGAAACGCACCTTGCGAGCGAAGGGTCTAGGCTCCGTTGAAGTCGACGGTCTGCTC
---------+---------+---------+---------+---------+---------+
C  G  K  R  T  L  R  A  K  G  L  G  S  V  E  V  D  G  L  L
```

FIG. 2.12

```
      3610                  3630                  3650
GACTCCGGCGCAGCTTGGACGCCTTGCCGCAACACCATCTTCTCTGCCGCCGTCATGCTC
---------+---------+---------+---------+---------+---------+
D  S  G  A  A  W  T  P  C  R  N  T  I  F  S  A  A  V  M  L

      3670                  3690                  3710
ACGCTCTTCCGCGGCGTCAAGTTCGCAGCTTTCAAAGGCGACGACTCGCTCCTCTGTGGT
---------+---------+---------+---------+---------+---------+
T  L  F  R  G  V  K  F  A  A  F  K  G  D  D  S  L  L  C  G

      3730                  3750                  3770
AGCCATTACCTCCGTTTCGACGCTAGCCGCCTTCACATGGGCGAACGTTACAAGACCAAA
---------+---------+---------+---------+---------+---------+
S  H  Y  L  R  F  D  A  S  R  L  H  M  G  E  R  Y  K  T  K

      3790                  3810                  3830
CATTTGAAGGTCGAGGTGCAGAAAATCGTGCCGTACATCGGACTCCTCGTCTCCGCTGAG
---------+---------+---------+---------+---------+---------+
H  L  K  V  E  V  Q  K  I  V  P  Y  I  G  L  L  V  S  A  E

      3850                  3870                  3890
CAGGTCGTCCTCGACCCTGTCAGGAGCGCTCTCAAGATATTTGGGCGCTGCTACACAAGC
---------+---------+---------+---------+---------+---------+
Q  V  V  L  D  P  V  R  S  A  L  K  I  F  G  R  C  Y  T  S
```

FIG. 2·13.

```
      3910                  3930                  3950
GAACTCCTTTACTCCAAGTACGTGGAGGCTGTGAGAGACATCACCAAGGGCTGGAGTGAC
---------+---------+---------+---------+---------+---------+
E  L  L  Y  S  K  Y  V  E  A  V  R  D  I  T  K  G  W  S  D

      3970                  3990                  4010
GCCCGCTACCACAGCCTCCTGTGCCACATGTCAGCATGCTACTACAATTACGCGCCGGAG
---------+---------+---------+---------+---------+---------+
A  R  Y  H  S  L  L  C  H  M  S  A  C  Y  Y  N  Y  A  P  E

      4030                  4050                  4070
TCTGCGGCGTACATCATCGACGCTGTTGTTCGCTTTGGGCGCGGCGACTTCCCGTTTGAA
---------+---------+---------+---------+---------+---------+
S  A  A  Y  I  I  D  A  V  V  R  F  G  R  G  D  F  P  F  E

      4090                  4110                  4130
CAACTGCGCGTGGTGCGTGCCCATGTGCAGGCACCCGACGCTTACAGCAGCACGTATCCG
---------+---------+---------+---------+---------+---------+
Q  L  R  V  V  R  A  H  V  Q  A  P  D  A  Y  S  S  T  Y  P

      4150                  4170                  4190
GCTAACGTGCGCGCATCGTGCCTTGACCACGTCTTCGAGCCCCGCCAGGCCGCCGCCCCG
---------+---------+---------+---------+---------+---------+
A  N  V  R  A  S  C  L  D  H  V  F  E  P  R  Q  A  A  A  P
```

FIG. 2·14

```
      4210                  4230                  4250
GCAGGTTTCGTTGCGACATGTGCGAAGCCGGAAACGCCTTCTTCACTTACCGCGAAAGCT
---------+---------+---------+---------+---------+---------+
A  G  F  V  A  T  C  A  K  P  E  T  P  S  S  L  T  A  K  A
                  M  C  E  A  G  N  A  F  F  T  Y  R  E  S  W
                  P11a start
      4270                  4290                  4310
GGTGTTTCTGCGACTACAAGCCACGTTGCGACTGGGACTGCGCCCCCGGAGTCTCCATGG
---------+---------+---------+---------+---------+---------+
G  V  S  A  T  T  S  H  V  A  T  G  T  A  P  P  E  S  P  W
   C  F  C  D  Y  K  P  R  C  D  W  D  C  A  P  G  V  S  M  G

      4330                  4350                  4370
GATGCACCTGCAGCCAACAGCTTTTCGGAGTTATTGACACCGGAGACCCCGTCCACATCA
---------+---------+---------+---------+---------+---------+
D  A  P  A  A  N  S  F  S  E  L  L  T  P  E  T  P  S  T  S
   C  T  C  S  Q  Q  L  F  G  V  I  D  T  G  D  P  V  H  I  I

      4390                  4410                  4430
TCCTCGCCGTCATCGTCTTCATCGGACTCCTCTACATCGTGTGGAAGGTCGCTCAGTGGT
---------+---------+---------+---------+---------+---------+
S  S  P  S  S  S  S  S  D  S  S  T  S  C  G  R  S  L  S  G
   L  A  V  I  V  F  I  G  L  L  Y  I  V  W  K  V  A  Q  W  W
```

FIG. 2-15

```
     4450                4470                4490
GGAGACACCGCAAGGACCACAGAAGACTTGAACAGCAGAAAGCCGCCTTCGCAAGACAGG
---------+---------+---------+---------+---------+---------+
G  D  T  A  R  T  T  E  D  L  N  S  R  K  P  P  S  Q  D  R
 R  H  R  K  D  H  R  R  L  E  Q  Q  K  A  A  F  A  R  Q  A

     4510                4530                4550
CAATCACGCTCGTCTGAATGTCTGGACAGAAGCGGAGAAAGGACAGGCAGTTCGTTAACT
---------+---------+---------+---------+---------+---------+
Q  S  R  S  S  E  C  L  D  R  S  G  E  R  T  G  S  S  L  T
 I  T  L  V  *  M  S  G  Q  K  R  R  K  D  R  Q  F  V  N  C
               P11b start
     4570                4590                4610
GCCCCCACTGCTCCGAGCCCCTCATTCTCATTTTCGGAAAGAGCTCGACTGGCGACCGGG
---------+---------+---------+---------+---------+---------+
A  P  T  A  P  S  P  S  F  S  F  S  E  R  A  R  L  A  T  G
 P  H  C  S  E  P  L  I  L  I  F  G  K  S  S  T  G  D  R  A

     4630                4650                4670
CCGACTGTCGCCGCTGCGACATCACCTTCGGCAACCCCATCCTGCGCCACGGACCAGGTT
---------+---------+---------+---------+---------+---------+
P  T  V  A  A  A  T  S  P  S  A  T  P  S  C  A  T  D  Q  V
 D  C  R  R  C  D  I  T  F  G  N  P  I  L  R  H  G  P  G  C
```

FIG. 2.16

```
      4690                  4710                  4730
GCCGCGAGGACCACGCCGGACTTTGCGCCTTTCCTGGGTTCCCAGTCTGCCCGTGCTGTC
---------+---------+---------+---------+---------+---------+
A  A  R  T  T  P  D  F  A  P  F  L  G  S  Q  S  A  R  A  V
   R  E  D  H  A  G  L  C  A  F  P  G  F  P  V  C  P  C  C  L

      4750                  4770                  4790
TCGAAGCCGTACCGGCCCCCCACGACTGCCCGTTGGAAAGAAGTCACCCCGCTCCACGCG
---------+---------+---------+---------+---------+---------+
S  K  P  Y  R  P  P  T  T  A  R  W  K  E  V  T  P  L  H  A
   E  A  V  P  A  P  H  D  C  P  L  E  R  S  H  P  A  P  R  V

      4810                  4830                  4850
TGGAAGGGCGTGACCGGAGACCGACCGGAAGTCAGGGAGGACCCGGAGACAGCGGCGGTC
---------+---------+---------+---------+---------+---------+
W  K  G  V  T  G  D  R  P  E  V  R  E  D  P  E  T  A  A  V
   E  G  R  D  R  R  P  T  G  S  Q  G  G  P  G  D  S  G  G  R

      4870                  4890                  4910
GTCCAGGCTCTGATCAGCGGCCGTTATCCTCAGAAGACGAAGCTTTCCTCCGACGCATCC
---------+---------+---------+---------+---------+---------+
V  Q  A  L  I  S  G  R  Y  P  Q  K  T  K  L  S  S  D  A  S
   P  G  S  D  Q  R  P  L  S  S  E  D  E  A  F  L  R  R  I  Q
```

FIG. 2.17

```
      4930                 4950                 4970
AAAGGCTACTCAAGAACTAAGGGATGCTCACAATCCACCTCTTTTCCTGCCCCGAGTGCG
---------+---------+---------+---------+---------+---------+
K  G  Y  S  R  T  K  G  C  S  Q  S  T  S  F  P  A  P  S  A
   R  L  L  K  N  *     M  L  T  I  H  L  F  S  C  P  E  C  G
                        P14 start
      4990                 5010                 5030
GATTACCAGGCCCGCGACTGCCAGACAGTCCGAGTCTGCCGCGCCGCTGCAGAGATGGCG
---------+---------+---------+---------+---------+---------+
D  Y  Q  A  R  D  C  Q  T  V  R  V  C  R  A  A  A  E  M  A
   L  P  G  P  R  L  P  D  S  P  S  L  P  R  R  C  R  D  G  A

      5050                 5070                 5090
CGCTCATGTATTCACGAGCCGTTGGCTTCATCTGCCGCCAGTGCCGACTTGAAGCGCATA
---------+---------+---------+---------+---------+---------+
R  S  C  I  H  E  P  L  A  S  S  A  A  S  A  D  L  K  R  I
   L  M  Y  S  R  A  V  G  F  I  C  R  Q  C  R  L  E  A  H  T

      5110                 5130                 5150
CGCTCTACCTCGGACTCTGTTCCCGATGTAAAGATCAGCAAGAGCGCATGAAGGAACAAA
---------+---------+---------+---------+---------+---------+
R  S  T  S  D  S  V  P  D  V  K  I  S  K  S  A  *
   L  Y  L  G  L  C  S  R  C  K  D  Q  Q  E  R  M  K  E  Q  N
```

FIG 2.18

```
      5170                  5190                  5210
ATTAGTTTCCTTGTTCGTAAACAAGGTGGTCCCTCCCATTGAGGTAAAGACTCTGGTGAG
---------+---------+---------+---------+---------+---------+
   *

      5230                  5250                  5270
TCCTCAACGTTACTCGTTGAGTCTGCTGCGGTTCGATTCCATTCCCAAGCAGCAAAGGGT
---------+---------+---------+---------+---------+---------+

      5290                  5310
GCGCAACTAGTACGGCGCCCCCTGGGATACCA
---------+---------+---------+--
```

FIG. 2.19.

```
         10                  30                  50
GTTTTTCTTTCTTTACCAAGTGTGGTAAAATTTAAACAAAGAAGAAAACCAGGACCGTAA
---------+---------+---------+---------+---------+---------+

         70                  90                 110
CCCGGCCCTTACACACCTCGAGTCCGTGACCACCGGATTATACGTCGCCCACCACACGGC
---------+---------+---------+---------+---------+---------+

        130                 150                 170
GCCTTTTCCGACCACTCTCGAGAGTCGTTGGGAGTTTCGTCCGTGACCACCCGGTTGGCA
---------+---------+---------+---------+---------+---------+

        190                 210                 230
GTCGACAGACGCTTCCGGACCACTAGAACCTCCTCGAGCGACGCACACACAGCACACACA
---------+---------+---------+---------+---------+---------+

        250                 270                 290
CCGCCTTAGCTGCACCTACGGCAGCGTTGATAGCGCGGATTTATGAGCGAGCACACCATC
---------+---------+---------+---------+---------+---------+
                                                M   S   E   H   T   I
                                                P17 start
        310                 330                 350
GCCCACTCCATCACATTACCACCCGGTTACACCCTTGCCCTAATACCCCCTGAACCTGAA
---------+---------+---------+---------+---------+---------+
A   H   S   I   T   L   P   P   G   Y   T   L   A   L   I   P   P   E   P   E
```

FIG. 3a.1

```
       370                 390                 410
GCAGGATGGGAGATGCTGGAGTGGCGTCACAGCGACCTCACAACCGTCGCGGAACCCGTA
---------+---------+---------+---------+---------+---------+
A  G  W  E  M  L  E  W  R  H  S  D  L  T  T  V  A  E  P  V
      M  G  D  A  G  V  A  S  Q  R  P  H  N  R  R  G  T  R  N
      P71 start
       430                 450                 470
ACGTTCGGGTCAGCGCCAACACCGTCACCGTCAATGGTAGAAGAAACCAACGGCGTCGGA
---------+---------+---------+---------+---------+---------+
T  F  G  S  A  P  T  P  S  P  S  M  V  E  E  T  N  G  V  G
   V  R  V  S  A  N  T  V  T  V  N  G  R  R  N  Q  R  R  R  T

       490                 510                 530
CCGGAAGGCAAGTTTCTCCCCCTGACAATTTCACCGCTGCTGCACAAGACCTCGCGCAAA
---------+---------+---------+---------+---------+---------+
P  E  G  K  F  L  P  L  T  I  S  P  L  L  H  K  T  S  R  K
   G  R  Q  V  S  P  P  D  N  F  T  A  A  A  Q  D  L  A  Q  S

       550                 570                 590
GCCTTGACGCCAACACCGTCACTTTCCCCGCTAACATCTCTAGCATGCCCGAATTCCGGA
---------+---------+---------+---------+---------+---------+
A  L  T  P  T  P  S  L  S  P  L  T  S  L  A  C  P  N  S  G
   L  D  A  N  T  V  T  F  P  A  N  I  S  S  M  P  E  F  R  N
```

FIG. 3a.2

```
       610                   630                   650
ATTGGGCCAAGGGAAAGATCGACCTCGACTCCGATTCCATCGGCTGGTACTTCAAGTACC
---------+---------+---------+---------+---------+---------+
I  G  P  R  E  R  S  T  S  T  P  I  P  S  A  G  T  S  S  T
  W  A  K  G  K  I  D  L  D  S  D  S  I  G  W  Y  F  K  Y  L

       670                   690                   710
TTGACCCAGCGGGTGCTACAGAGTCTGCGCGCGCCGTCGGCGAGTACTCGAAGATCCCTG
---------+---------+---------+---------+---------+---------+
L  T  Q  R  V  L  Q  S  L  R  A  P  S  A  S  T  R  R  S  L
  D  P  A  G  A  T  E  S  A  R  A  V  G  E  Y  S  K  I  P  D

       730                   750                   770
ACGGCCTCGTCAAGTTCTCCGTCGACGCAGAGATAAGAGAGATCTATAACGAGGAGTGCC
---------+---------+---------+---------+---------+---------+
T  A  S  S  S  S  P  S  T  Q  R  *
  G  L  V  K  F  S  V  D  A  E  I  R  E  I  Y  N  E  E  C  P

       790                   810                   830
CCGTCGTCACTGACGTGTCCGTCCCCCTCGACGGCCGCCAGTGGAGCCTCTCGATTTTCT
---------+---------+---------+---------+---------+---------+
  V  V  T  D  V  S  V  P  L  D  G  R  Q  W  S  L  S  I  F  S
```

FIG. 3a-3

```
       850                       870                       890
CCTTTCCGATGTTCAGAACCGCCTACGTCGCCGTAGCGAACGTCGAGAACAAGGAGATGT
---------+---------+---------+---------+---------+---------+
  F  P  M  F  R  T  A  Y  V  A  V  A  N  V  E  N  K  E  M  S

       910                       930                       950
CGCTCGACGTTGTCAACGACCTCATCGAGTGGCTCAACAATCTCGCCGACTGGCGTTATG
---------+---------+---------+---------+---------+---------+
  L  D  V  V  N  D  L  I  E  W  L  N  N  L  A  D  W  R  Y  V

       970                       990                      1010
TCGTTGACTCTGAACAGTGGATTAACTTCACCAATGACACCACGTACTACGTCCGCATCC
---------+---------+---------+---------+---------+---------+
  V  D  S  E  Q  W  I  N  F  T  N  D  T  T  Y  Y  V  R  I  R

      1030                      1050                      1070
GCGTTCTACGTCCAACCTACGACGTTCCAGACCCCACAGAGGGCCTTGTTCGCACAGTCT
---------+---------+---------+---------+---------+---------+
  V  L  R  P  T  Y  D  V  P  D  P  T  E  G  L  V  R  T  V  S

      1090                      1110                      1130
CAGACTACCGCCTCACTTATAAGGCGATAACATGTGAAGCCAACATGCCAACACTCGTCG
---------+---------+---------+---------+---------+---------+
  D  Y  R  L  T  Y  K  A  I  T  C  E  A  N  M  P  T  L  V  D
```

FIG. 3a:4

```
      1150                1170                1190
ACCAAGGCTTTTGGATCGGCGGCCAGTACGCTCTCACCCCGACTAGCCTACCGCAGTACG
---------+---------+---------+---------+---------+---------+
  Q  G  F  W  I  G  G  Q  Y  A  L  T  P  T  S  L  P  Q  Y  D

      1210                1230                1250
ACGTCAGCGAGGCCTACGCTCTGCACACTTTGACCTTCGCCAGACCATCCAGCGCCGCTG
---------+---------+---------+---------+---------+---------+
  V  S  E  A  Y  A  L  H  T  L  T  F  A  R  P  S  S  A  A  A

      1270                1290                1310
CACTCGCGTTTGTGTGGGCAGGTTTGCCACAGGGTGGCACTGCGCCTGCAGGCACTCCAG
---------+---------+---------+---------+---------+---------+
  L  A  F  V  W  A  G  L  P  Q  G  G  T  A  P  A  G  T  P  A

      1330                1350                1370
CCTGGGAGCAGGCATCCTCGGGTGGCTACCTCACCTGGCGCCACAACGGTACTACTTTCC
---------+---------+---------+---------+---------+---------+
  W  E  Q  A  S  S  G  G  Y  L  T  W  R  H  N  G  T  T  F  P

      1390                1410                1430
CAGCTGGCTCCGTTAGCTACGTTCTCCCTGAGGGTTTCGCCCTTGAGCGCTACGACCCGA
---------+---------+---------+---------+---------+---------+
  A  G  S  V  S  Y  V  L  P  E  G  F  A  L  E  R  Y  D  P  N
```

FIG 3a.5

```
      1450                 1470                 1490
ACGACGGCTCTTGGACCGACTTCGCTTCCGCAGGAGACACCGTCACTTTCCGGCAGGTCG
---------+---------+---------+---------+---------+---------+
  D  G  S  W  T  D  F  A  S  A  G  D  T  V  T  F  R  Q  V  A

      1510                 1530                 1550
CCGTCGACGAGGTCGTTGTGACCAACAACCCCGCCGGCGGCGGCAGCGCCCCCACCTTCA
---------+---------+---------+---------+---------+---------+
  V  D  E  V  V  V  T  N  N  P  A  G  G  G  S  A  P  T  F  T

      1570                 1590                 1610
CCGTGAGAGTGCCCCCTTCAAACGCTTACACCAACACCGTGTTTAGGAACACGCTCTTAG
---------+---------+---------+---------+---------+---------+
  V  R  V  P  P  S  N  A  Y  T  N  T  V  F  R  N  T  L  L  E

      1630                 1650                 1670
AGACTCGACCCTCCTCTCGTAGGCTCGAACTCCCTATGCCACCTGCTGACTTTGGACAGA
---------+---------+---------+---------+---------+---------+
  T  R  P  S  S  R  R  L  E  L  P  M  P  P  A  D  F  G  Q  T

      1690                 1710                 1730
CGGTCGCCAACAACCCGAAGATCGAGCAGTCGCTTCTTAAAGAAACACTTGGCTGCTATT
---------+---------+---------+---------+---------+---------+
  V  A  N  N  P  K  I  E  Q  S  L  L  K  E  T  L  G  C  Y  L
```

FIG. 3a.6

```
      1750                  1770                  1790
TGGTCCACTCCAAAATGCGAAACCCCGTTTTCCAGCTCACGCCAGCCAGCTCCTTTGGCG
---------+---------+---------+---------+---------+---------+
  V  H  S  K  M  R  N  P  V  F  Q  L  T  P  A  S  S  F  G  A

      1810                  1830                  1850
CCGTTTCCTTCAACAATCCGGGTTATGAGCGCACACGCGACCTCCCGGACTACACTGGCA
---------+---------+---------+---------+---------+---------+
  V  S  F  N  N  P  G  Y  E  R  T  R  D  L  P  D  Y  T  G  I

      1870                  1890                  1910
TCCGTGACTCATTCGACCAGAACATGTCCACCGCTGTGGCCCACTTCCGCTCACTCTCCC
---------+---------+---------+---------+---------+---------+
  R  D  S  F  D  Q  N  M  S  T  A  V  A  H  F  R  S  L  S  H

      1930                  1950                  1970
ACTCCTGCAGTATCGTCACTAAGACCTACCAGGGTTGGGAAGGCGTCACGAACGTCAACA
---------+---------+---------+---------+---------+---------+
  S  C  S  I  V  T  K  T  Y  Q  G  W  E  G  V  T  N  V  N  T

      1990                  2010                  2030
CGCCTTTCGGCCAATTCGCGCACGCGGGCCTCCTCAAGAATGAGGAGATCCTCTGCCTCG
---------+---------+---------+---------+---------+---------+
  P  F  G  Q  F  A  H  A  G  L  L  K  N  E  E  I  L  C  L  A
```

FIG 3a-7

```
      2050                 2070                 2090
CCGACGACCTGGCCACCCGTCTCACAGGTGTCTACCCCGCCACTGACAACTTCGCGGCCG
---------+---------+---------+---------+---------+---------+
  D  D  L  A  T  R  L  T  G  V  Y  P  A  T  D  N  F  A  A  A

      2110                 2130                 2150
CCGTTTCTGCCTTCGCCGCGAACATGCTGTCCTCCGTGCTGAAGTCGGAGGCAACGTCCT
---------+---------+---------+---------+---------+---------+
  V  S  A  F  A  A  N  M  L  S  S  V  L  K  S  E  A  T  S  S

      2170                 2190                 2210
CCATCATCAAGTCCGTTGGCGAGACTGCCGTCGGCGCGGCTCAGTCCGGCCTCGCGAAGC
---------+---------+---------+---------+---------+---------+
  I  I  K  S  V  G  E  T  A  V  G  A  A  Q  S  G  L  A  K  L

      2230                 2250                 2270
TACCCGGACTGCTAATGAGTGTACCAGGGAAGATTGCCGCGCGTGTCCGCGCGCGCCGAG
---------+---------+---------+---------+---------+---------+
  P  G  L  L  M  S  V  P  G  K  I  A  A  R  V  R  A  R  R  A

      2290                 2310                 2330
CGCGCCGCCGCGCCGCTCGTGCCAATTAGTTTGCTCGCTCCTGTTTCGCCGTTTCGTAAA
---------+---------+---------+---------+---------+---------+
  R  R  R  A  A  R  A  N  *
```

FIG. 3a-8

```
      2350                  2370                  2390
ACGGCGTGGTCCCGCACATTACGCGTACCCTAAAGACTCTGGTGAGTCCCCGTCGTTACA
---------+---------+---------+---------+---------+---------+

      2410                  2430                  2450
CGACGGGTCTGCCGCGGTTCGATTCCATTCCCAAGCGGCAAGAAGGACGTAGTTAGCTCT
---------+---------+---------+---------+---------+---------+

      2470
GCGTCCCTCGGGATACCA
---------+--------
```

FIG. 3a.9

```
         10                  30                  50
GTTTTTCTTTCTTTACCAAGTGTGGTAAAATTTAAACAAAGAAGAAAACCAGGACCGTAA
---------+---------+---------+---------+---------+---------+

         70                  90                 110
CCCGGCCCTTACACACCTCGAGTCCGTGACCACCGGATTATACGTCGCCCACCACACGGC
---------+---------+---------+---------+---------+---------+

        130                 150                 170
GCCTTTTCCGACCACTCTCGAGAGTCGTTGGGAGTTTCGTCCGTGACCACCCGGTTGGCA
---------+---------+---------+---------+---------+---------+

        190                 210                 230
GTCGACAGACGCTTCCGGACCACTAGAACCTCCTCGAGCGACGCACACACAGCACACACA
---------+---------+---------+---------+---------+---------+

        250                 270                 290
CCGCCTTAGCTGCACCTACGGCAGCGTTGATAGCGCGGATTTATGAGCGAGCACACCATC
---------+---------+---------+---------+---------+---------+
                                              M   S   E   H   T   I
                                    "P70" fusion protein start
        310                 330                 350
GCCCACTCCATCACATTACCACCCGGTTACACCCTTGCCCTAATACCCCCTGAACCTGAA
---------+---------+---------+---------+---------+---------+
A   H   S   I   T   L   P   P   G   Y   T   L   A   L   I   P   P   E   P   E
```

FIG. 36!

```
        370                 390                 410
GCAGGATGGGAGATGCTGGAGTGGCGTCACAGCGACCTCACAACCGTCGCGGAACCCGTA
---------+---------+---------+---------+---------+---------+
A  G  W  E  M  L  E  W  R  H  S  D  L  T  T  V  A  E  P  V

        430                 450                 470
ACGTTCGGGTCAGCGCCAACACCGTCACCGTCAATGGTAGAAGAAACCAACGGCGTCGGA
---------+---------+---------+---------+---------+---------+
T  F  G  S  A  P  T  P  S  P  S  M  V  E  E  T  N  G  V  G

        490                 510                 530
CCGGAAGGCAAGTTTCTCCCCCTGACAATTTCACCGCTGCTGCACAAGACCTCGCGCAAA
---------+---------+---------+---------+---------+---------+
P  E  G  K  F  L  P  L  T  I  S  P  L  L  H  K  T  S  R  K

        550                 570                 590
GCCTTGACGCCAACACCGTCACTTTCCCCCGCTAACATCTCTAGCATGCCCGAATTCCGG
---------+---------+---------+---------+---------+---------+
A  L  T  P  T  P  S  L  S  P  A  N  I  S  S  M  P  E  F  R

        610                 630                 650
AATTGGGCCAAGGGAAAGATCGACCTCGACTCCGATTCCATCGGCTGGTACTTCAAGTAC
---------+---------+---------+---------+---------+---------+
N  W  A  K  G  K  I  D  L  D  S  D  S  I  G  W  Y  F  K  Y
```

FIG. 3b-2

```
        670                       690                       710
CTTGACCCAGCGGGTGCTACAGAGTCTGCGCGCGCCGTCGGCGAGTACTCGAAGATCCCT
---------+---------+---------+---------+---------+---------+---------+
L  D  P  A  G  A  T  E  S  A  R  A  V  G  E  Y  S  K  I  P

        730                       750                       770
GACGGCCTCGTCAAGTTCTCCGTCGACGCAGAGATAAGAGAGATCTATAACGAGGAGTGC
---------+---------+---------+---------+---------+---------+---------+
D  G  L  V  K  F  S  V  D  A  E  I  R  E  I  Y  N  E  E  C

        790                       810                       830
CCCGTCGTCACTGACGTGTCCGTCCCCCTCGACGGCCGCCAGTGGAGCCTCTCGATTTTC
---------+---------+---------+---------+---------+---------+---------+
P  V  V  T  D  V  S  V  P  L  D  G  R  Q  W  S  L  S  I  F

        850                       870                       890
TCCTTTCCGATGTTCAGAACCGCCTACGTCGCCGTAGCGAACGTCGAGAACAAGGAGATG
---------+---------+---------+---------+---------+---------+---------+
S  F  P  M  F  R  T  A  Y  V  A  V  A  N  V  E  N  K  E  M

        910                       930                       950
TCGCTCGACGTTGTCAACGACCTCATCGAGTGGCTCAACAATCTCGCCGACTGGCGTTAT
---------+---------+---------+---------+---------+---------+---------+
S  L  D  V  V  N  D  L  I  E  W  L  N  N  L  A  D  W  R  Y
```

FIG. 3b.3

```
       970                       990                      1010
GTCGTTGACTCTGAACAGTGGATTAACTTCACCAATGACACCACGTACTACGTCCGCATC
---------+---------+---------+---------+---------+---------+
V  V  D  S  E  Q  W  I  N  F  T  N  D  T  T  Y  Y  V  R  I

       1030                      1050                     1070
CGCGTTCTACGTCCAACCTACGACGTTCCAGACCCCACAGAGGGCCTTGTTCGCACAGTC
---------+---------+---------+---------+---------+---------+
R  V  L  R  P  T  Y  D  V  P  D  P  T  E  G  L  V  R  T  V

       1090                      1110                     1130
TCAGACTACCGCCTCACTTATAAGGCGATAACATGTGAAGCCAACATGCCAACACTCGTC
---------+---------+---------+---------+---------+---------+
S  D  Y  R  L  T  Y  K  A  I  T  C  E  A  N  M  P  T  L  V

       1150                      1170                     1190
GACCAAGGCTTTTGGATCGGCGGCCAGTACGCTCTCACCCCGACTAGCCTACCGCAGTAC
---------+---------+---------+---------+---------+---------+
D  Q  G  F  W  I  G  G  Q  Y  A  L  T  P  T  S  L  P  Q  Y

       1210                      1230                     1250
GACGTCAGCGAGGCCTACGCTCTGCACACTTTGACCTTCGCCAGACCATCCAGCGCCGCT
---------+---------+---------+---------+---------+---------+
D  V  S  E  A  Y  A  L  H  T  L  T  F  A  R  P  S  S  A  A
```

FIG. 36.4

```
      1270                1290                1310
GCACTCGCGTTTGTGTGGGCAGGTTTGCCACAGGGTGGCACTGCGCCTGCAGGCACTCCA
---------+---------+---------+---------+---------+---------+
A  L  A  F  V  W  A  G  L  P  Q  G  G  T  A  P  A  G  T  P

      1330                1350                1370
GCCTGGGAGCAGGCATCCTCGGGTGGCTACCTCACCTGGCGCCACAACGGTACTACTTTC
---------+---------+---------+---------+---------+---------+
A  W  E  Q  A  S  S  G  G  Y  L  T  W  R  H  N  G  T  T  F

      1390                1410                1430
CCAGCTGGCTCCGTTAGCTACGTTCTCCCTGAGGGTTTCGCCCTTGAGCGCTACGACCCG
---------+---------+---------+---------+---------+---------+
P  A  G  S  V  S  Y  V  L  P  E  G  F  A  L  E  R  Y  D  P

      1450                1470                1490
AACGACGGCTCTTGGACCGACTTCGCTTCCGCAGGAGACACCGTCACTTTCCGGCAGGTC
---------+---------+---------+---------+---------+---------+
N  D  G  S  W  T  D  F  A  S  A  G  D  T  V  T  F  R  Q  V

      1510                1530                1550
GCCGTCGACGAGGTCGTTGTGACCAACAACCCCGCCGGCGGCGGCAGCGCCCCCACCTTC
---------+---------+---------+---------+---------+---------+
A  V  D  E  V  V  V  T  N  N  P  A  G  G  G  S  A  P  T  F
```

FIG. 36.5

```
      1570                 1590                 1610
ACCGTGAGAGTGCCCCCTTCAAACGCTTACACCAACACCGTGTTTAGGAACACGCTCTTA
---------+---------+---------+---------+---------+---------+
T  V  R  V  P  P  S  N  A  Y  T  N  T  V  F  R  N  T  L  L

      1630                 1650                 1670
GAGACTCGACCCTCCTCTCGTAGGCTCGAACTCCCTATGCCACCTGCTGACTTTGGACAG
---------+---------+---------+---------+---------+---------+
E  T  R  P  S  S  R  R  L  E  L  P  M  P  P  A  D  F  G  Q

      1690                 1710                 1730
ACGGTCGCCAACAACCCGAAGATCGAGCAGTCGCTTCTTAAAGAAACACTTGGCTGCTAT
---------+---------+---------+---------+---------+---------+
T  V  A  N  N  P  K  I  E  Q  S  L  L  K  E  T  L  G  C  Y

      1750                 1770                 1790
TTGGTCCACTCCAAAATGCGAAACCCCGTTTTCCAGCTCACGCCAGCCAGCTCCTTTGGC
---------+---------+---------+---------+---------+---------+
L  V  H  S  K  M  R  N  P  V  F  Q  L  T  P  A  S  S  F  G

      1810                 1830                 1850
GCCGTTTCCTTCAACAATCCGGGTTATGAGCGCACACGCGACCTCCCGGACTACACTGGC
---------+---------+---------+---------+---------+---------+
A  V  S  F  N  N  P  G  Y  E  R  T  R  D  L  P  D  Y  T  G
```

FIG. 3b.6

```
      1870                 1890                 1910
ATCCGTGACTCATTCGACCAGAACATGTCCACCGCTGTGGCCCACTTCCGCTCACTCTCC
---------+---------+---------+---------+---------+---------+
I  R  D  S  F  D  Q  N  M  S  T  A  V  A  H  F  R  S  L  S

      1930                 1950                 1970
CACTCCTGCAGTATCGTCACTAAGACCTACCAGGGTTGGGAAGGCGTCACGAACGTCAAC
---------+---------+---------+---------+---------+---------+
H  S  C  S  I  V  T  K  T  Y  Q  G  W  E  G  V  T  N  V  N

      1990                 2010                 2030
ACGCCTTTCGGCCAATTCGCGCACGCGGGCCTCCTCAAGAATGAGGAGATCCTCTGCCTC
---------+---------+---------+---------+---------+---------+
T  P  F  G  Q  F  A  H  A  G  L  L  K  N  E  E  I  L  C  L

      2050                 2070                 2090
GCCGACGACCTGGCCACCCGTCTCACAGGTGTCTACCCCGCCACTGACAACTTCGCGGCC
---------+---------+---------+---------+---------+---------+
A  D  D  L  A  T  R  L  T  G  V  Y  P  A  T  D  N  F  A  A

      2110                 2130                 2150
GCCGTTTCTGCCTTCGCCGCGAACATGCTGTCCTCCGTGCTGAAGTCGGAGGCAACGTCC
---------+---------+---------+---------+---------+---------+
A  V  S  A  F  A  A  N  M  L  S  S  V  L  K  S  E  A  T  S
```

FIG. 36.7

```
      2170                2190                2210
TCCATCATCAAGTCCGTTGGCGAGACTGCCGTCGGCGCGGCTCAGTCCGGCCTCGCGAAG
---------+---------+---------+---------+---------+---------+
S  I  I  K  S  V  G  E  T  A  V  G  A  A  Q  S  G  L  A  K

      2230                2250                2270
CTACCCGGACTGCTAATGAGTGTACCAGGGAAGATTGCCGCGCGTGTCCGCGCGCGCCGA
---------+---------+---------+---------+---------+---------+
L  P  G  L  L  M  S  V  P  G  K  I  A  A  R  V  R  A  R  R

      2290                2310                2330
GCGCGCCGCCGCGCCGCTCGTGCCAATTAGTTTGCTCGCTCCTGTTTCGCCGTTTCGTAA
---------+---------+---------+---------+---------+---------+
A  R  R  R  A  A  R  A  N  *

      2350                2370                2390
AACGGCGTGGTCCCGCACATTACGCGTACCCTAAAGACTCTGGTGAGTCCCCGTCGTTAC
---------+---------+---------+---------+---------+---------+

      2410                2430                2450
ACGACGGGTCTGCCGCGGTTCGATTCCATTCCCAAGCGGCAAGAAGGACGTAGTTAGCTC
---------+---------+---------+---------+---------+---------+

      2470
TGCGTCCCTCGGGATACCA
---------+---------
```

FIG 3b.8

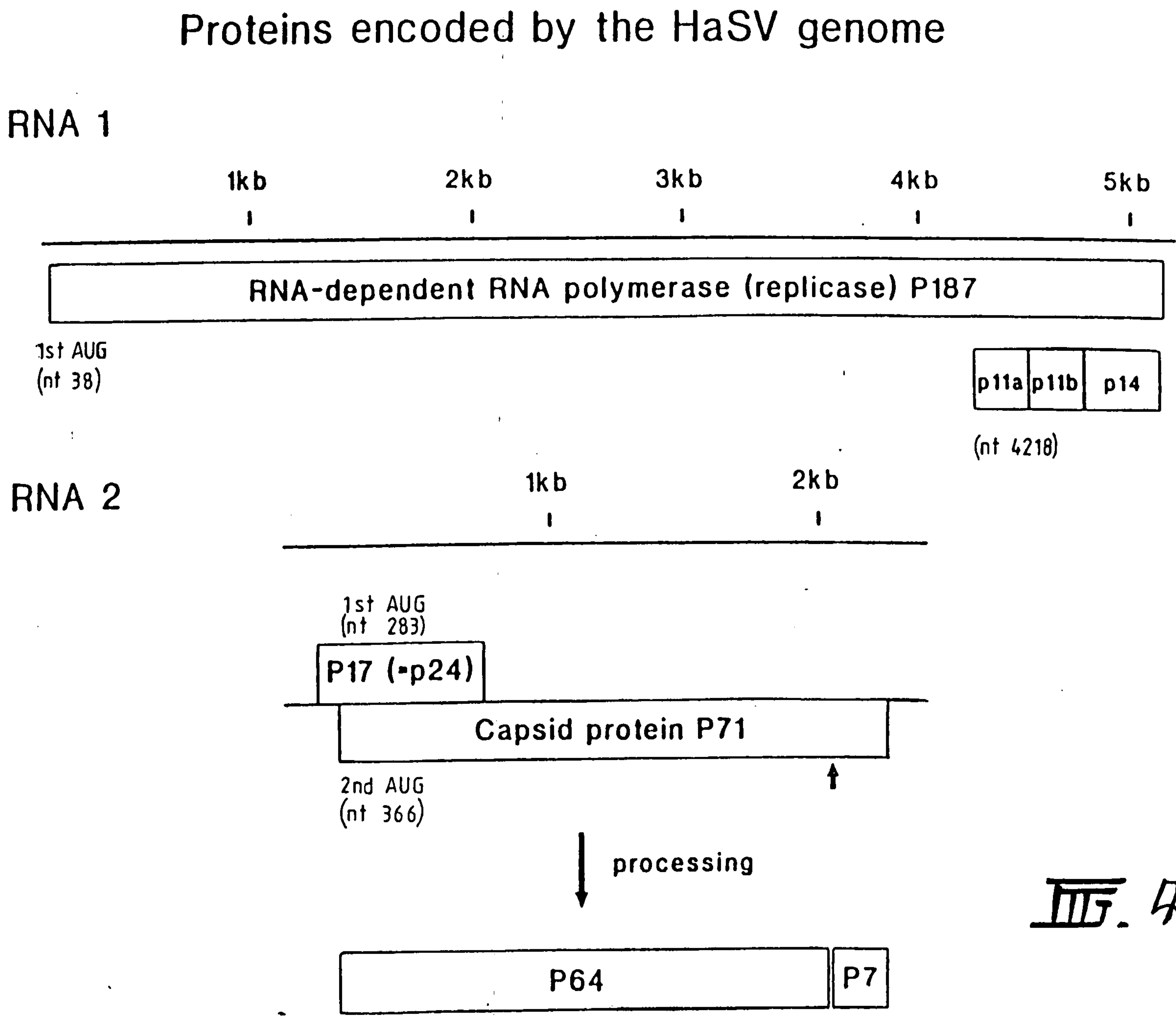


FIG. 4.

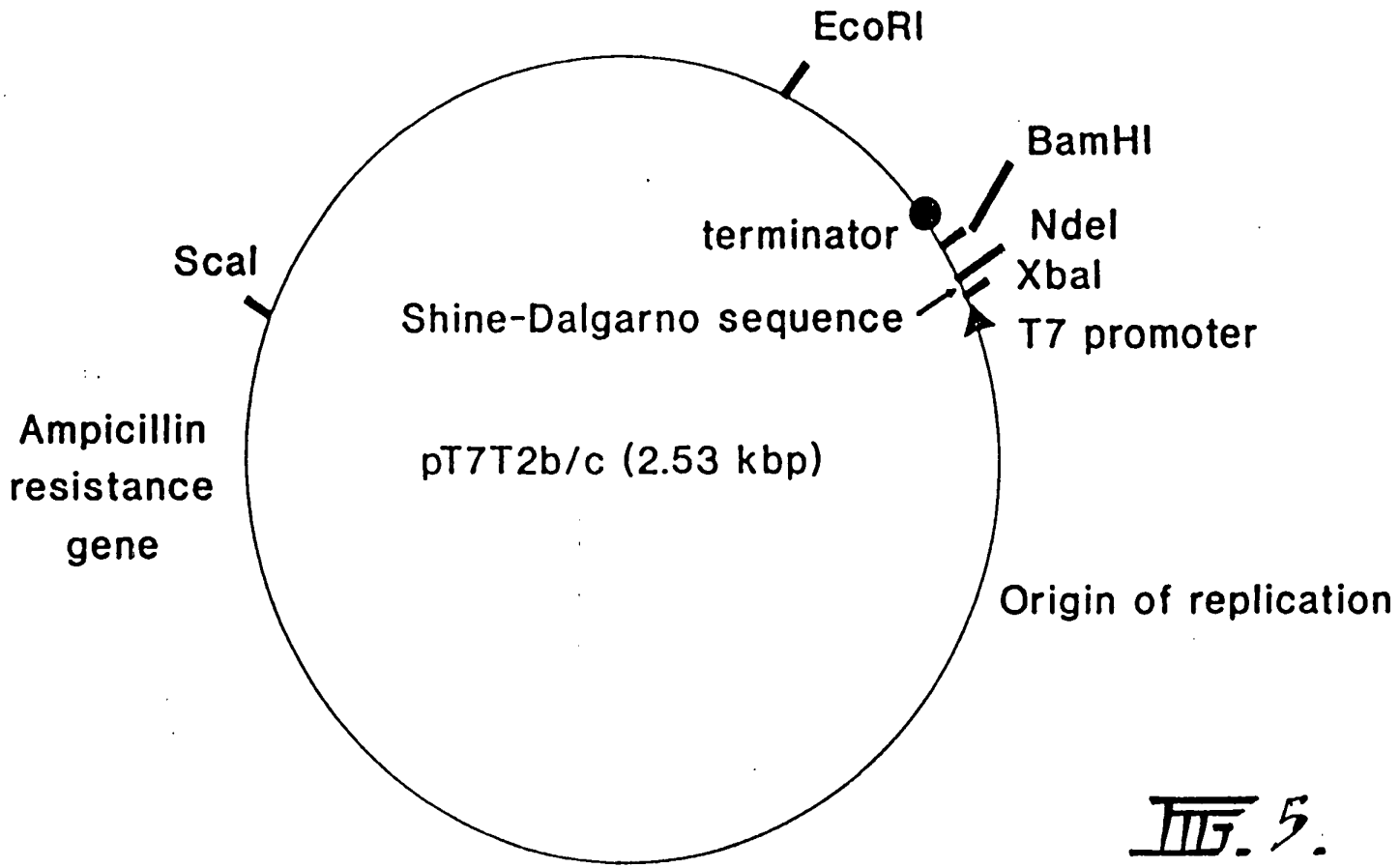
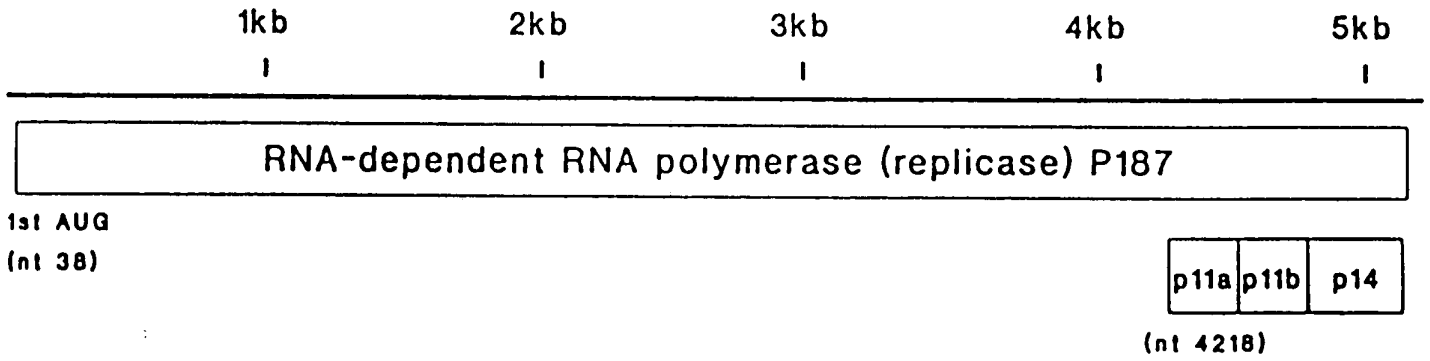

EcoRI
BamHI
terminator
NdeI
XbaI
ScaI
Shine-Dalgarno sequence
T7 promoter
Ampicillin
resistance
gene
pT7T2b/c (2.53 kbp)
Origin of replication

FIG. 5.

Proteins encoded by the HaSV genome

RNA 1



RNA 2

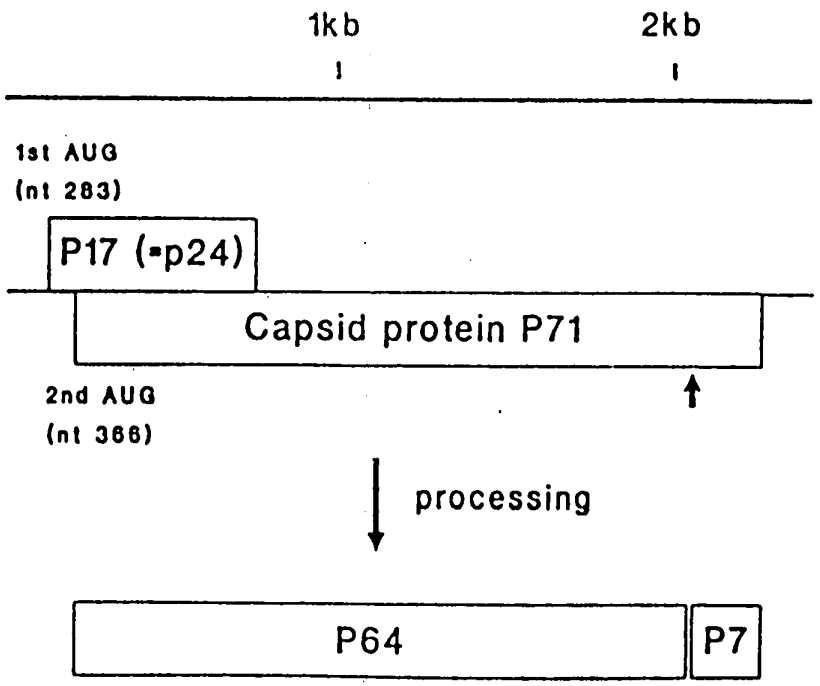


FIG. 6.

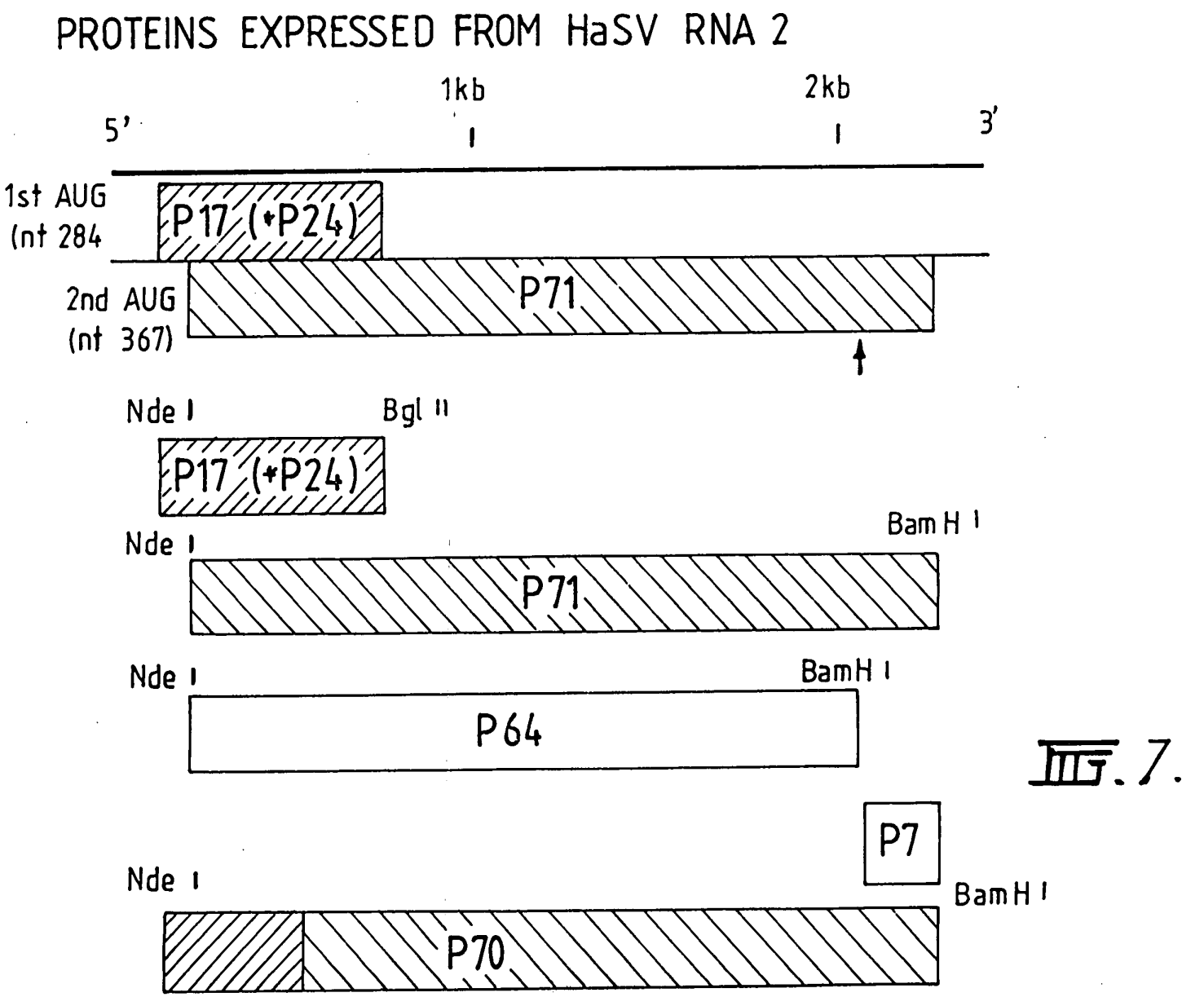


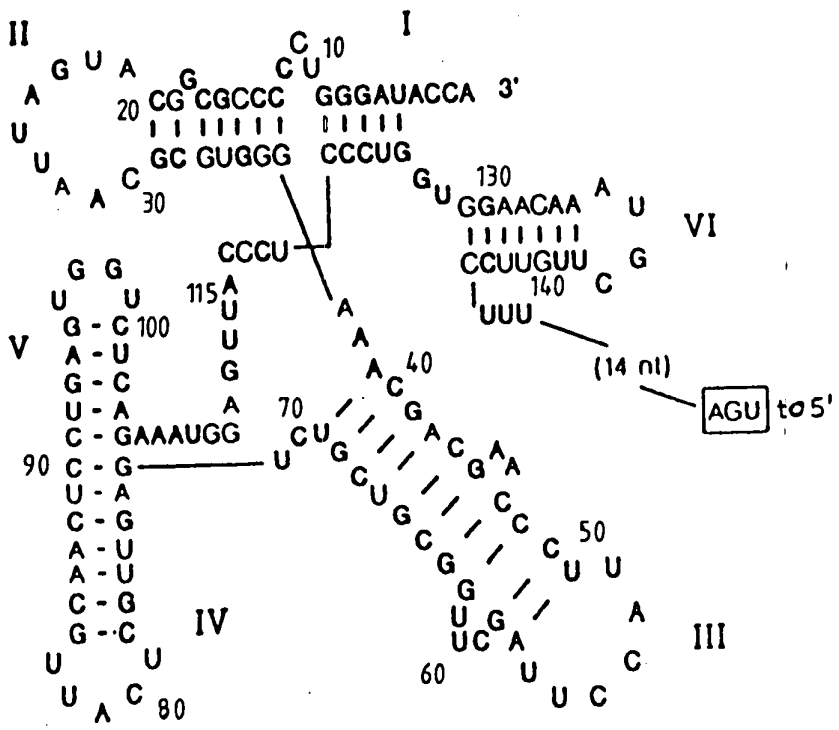
FIG. 7.

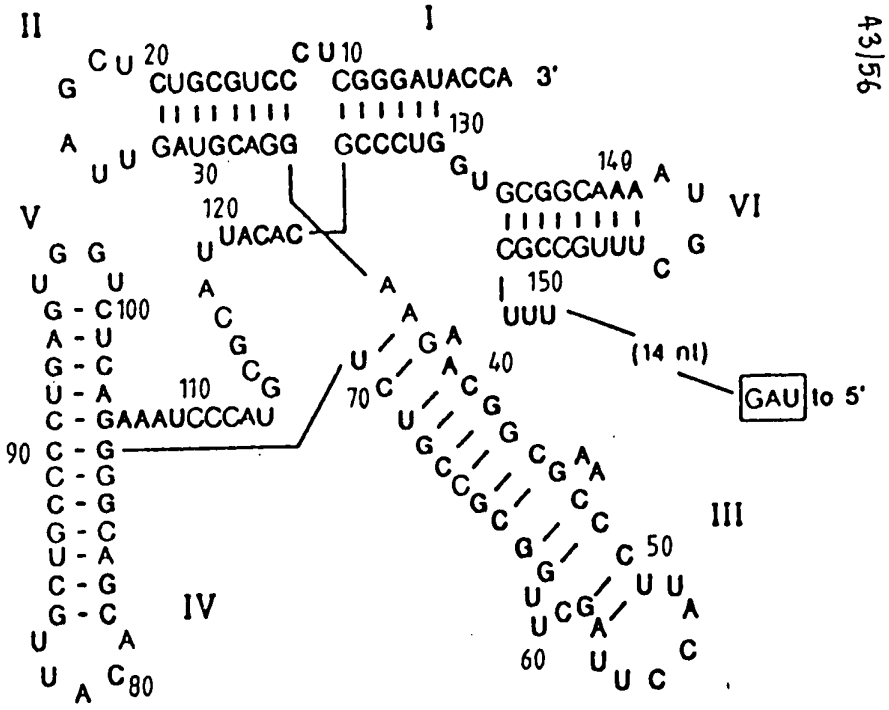
HaSV RNA 3' - terminal tRNA-like structures

RNA 1

RNA 2

FIG. 8.





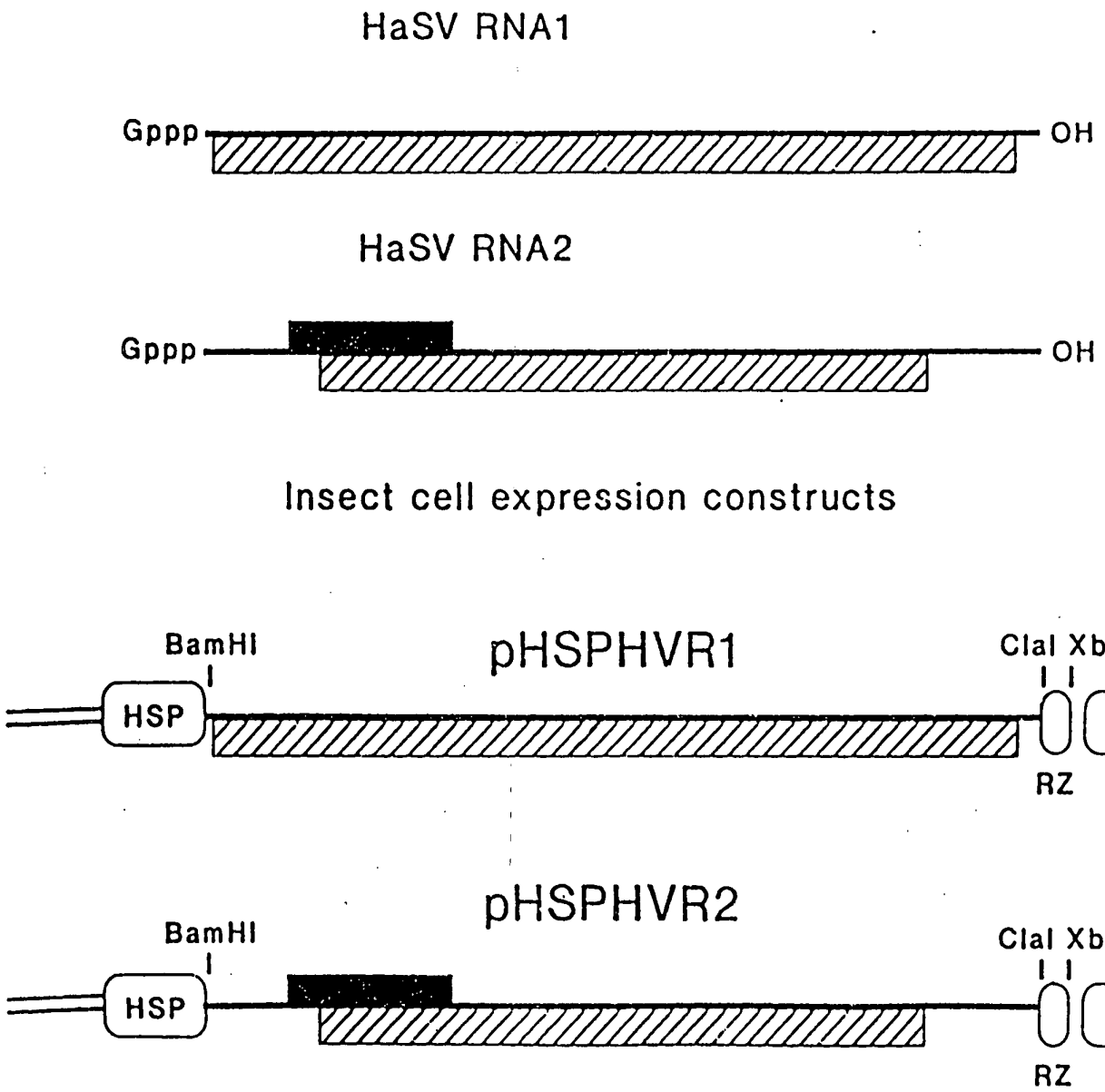
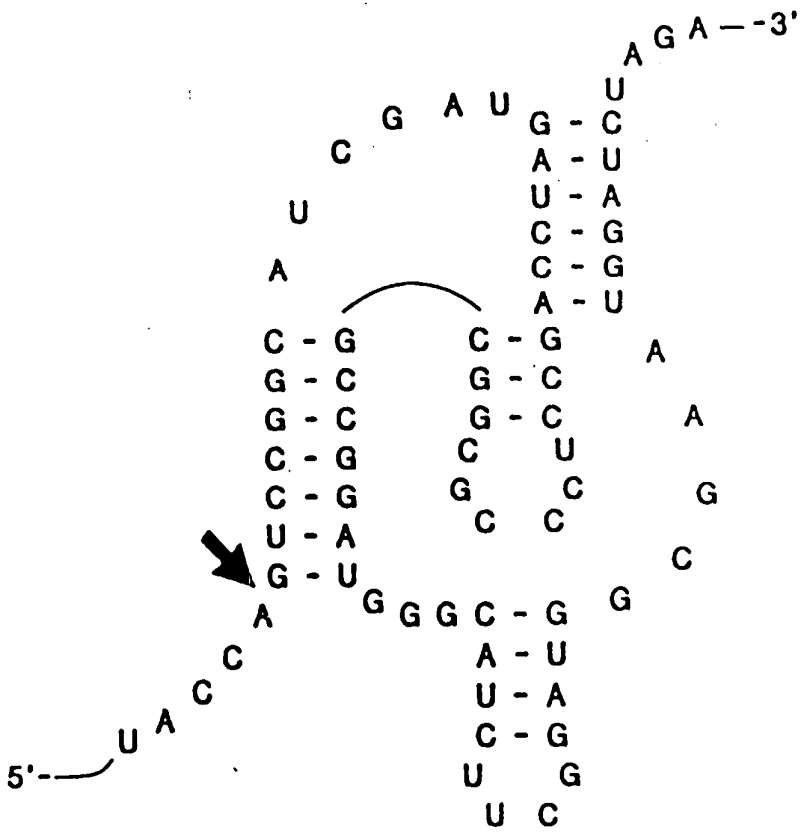

HaSV RNA1
Gppp
OH
HaSV RNA2
Gppp
OH
Insect cell expression constructs
BamHI
pHSPHVR1
ClaI XbaI
HSP
pA
RZ
pHSPHVR2
BamHI
ClaI XbaI
HSP
pA
RZ

FIG. 9.

CIS-ACTING RIBOZYMES FOR HASV 3' ENDS

HEPATITIS DELTA VIRUS



HAIRPIN

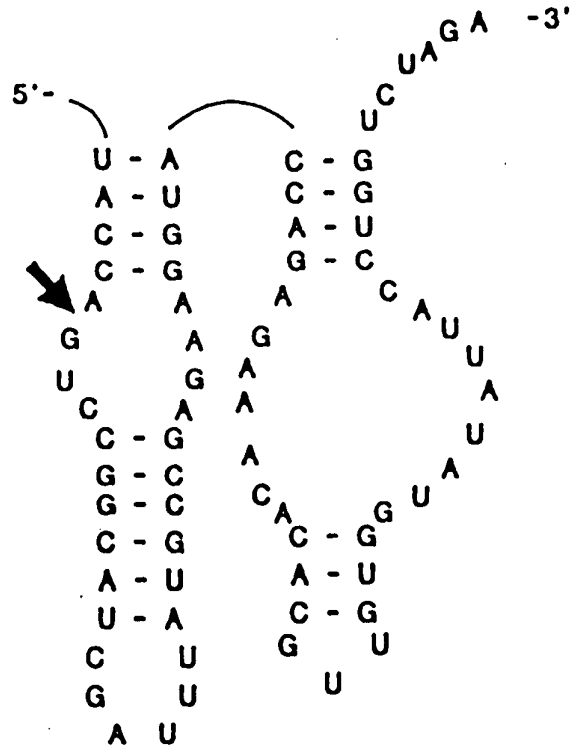
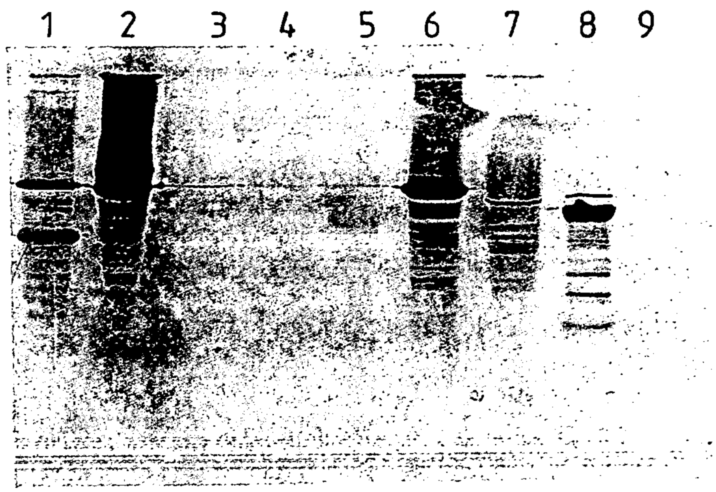


FIG. 10.

FIG. 11.

WESTERN BLOTS OF HaSV CAPSID PROTEIN

A. HaSV ANTISERUM



B. HaSV ANTISERUM

C. Bt ANTISERUM

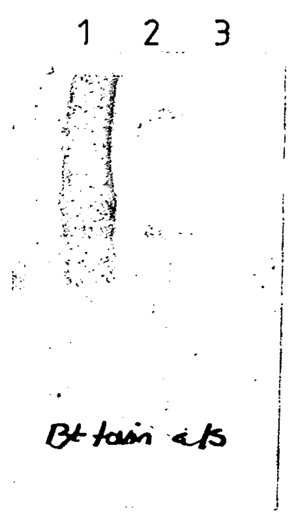
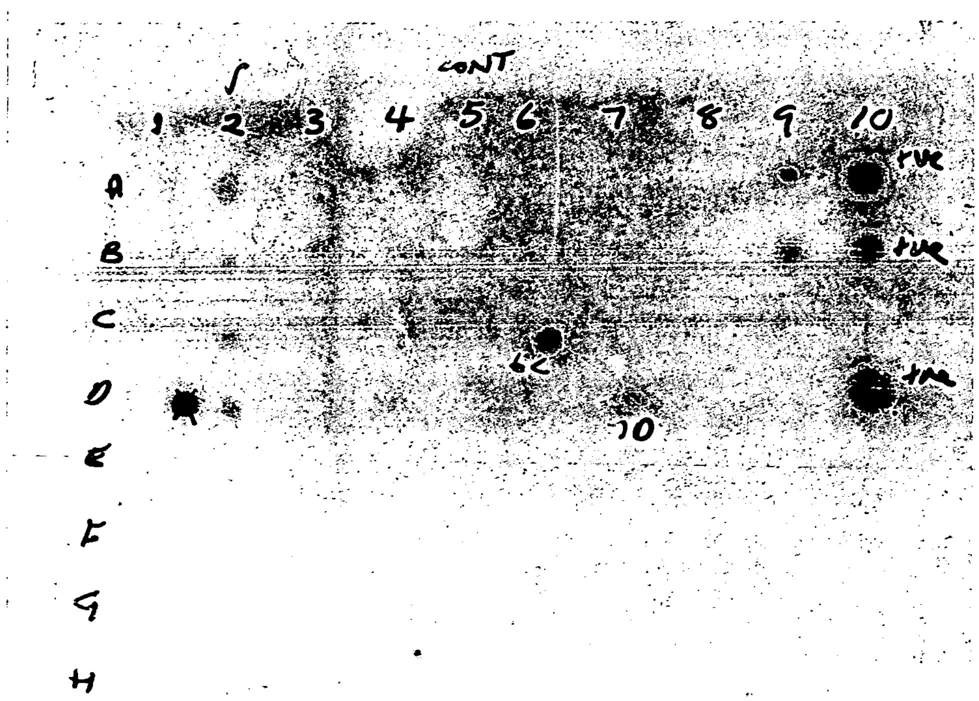


FIG. 12.

DOT-BLOT DETECTION OF HaSV IN FIELD-COLLECTED HELICOVERPA LARVAE



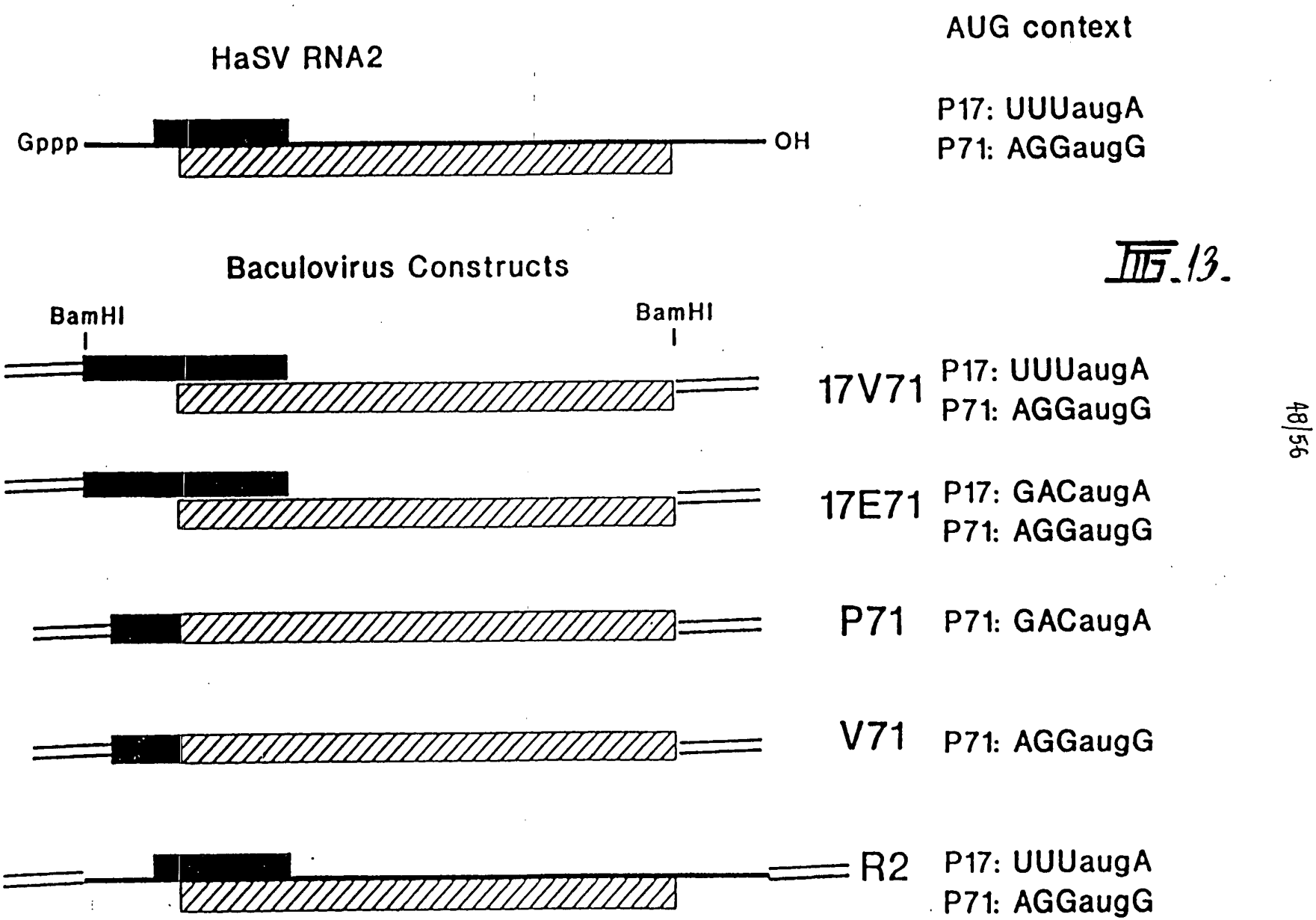

HaSV RNA2
AUG context
Gppp
OH
P17: UUUaugA
P71: AGGaugG
Baculovirus Constructs
BamHI
BamHI
17V71
P17: UUUaugA
P71: AGGaugG
17E71
P17: GACaugA
P71: AGGaugG
P71
P71: GACaugA
V71
P71: AGGaugG
R2
P17: UUUaugA
P71: AGGaugG

FIG. 13.

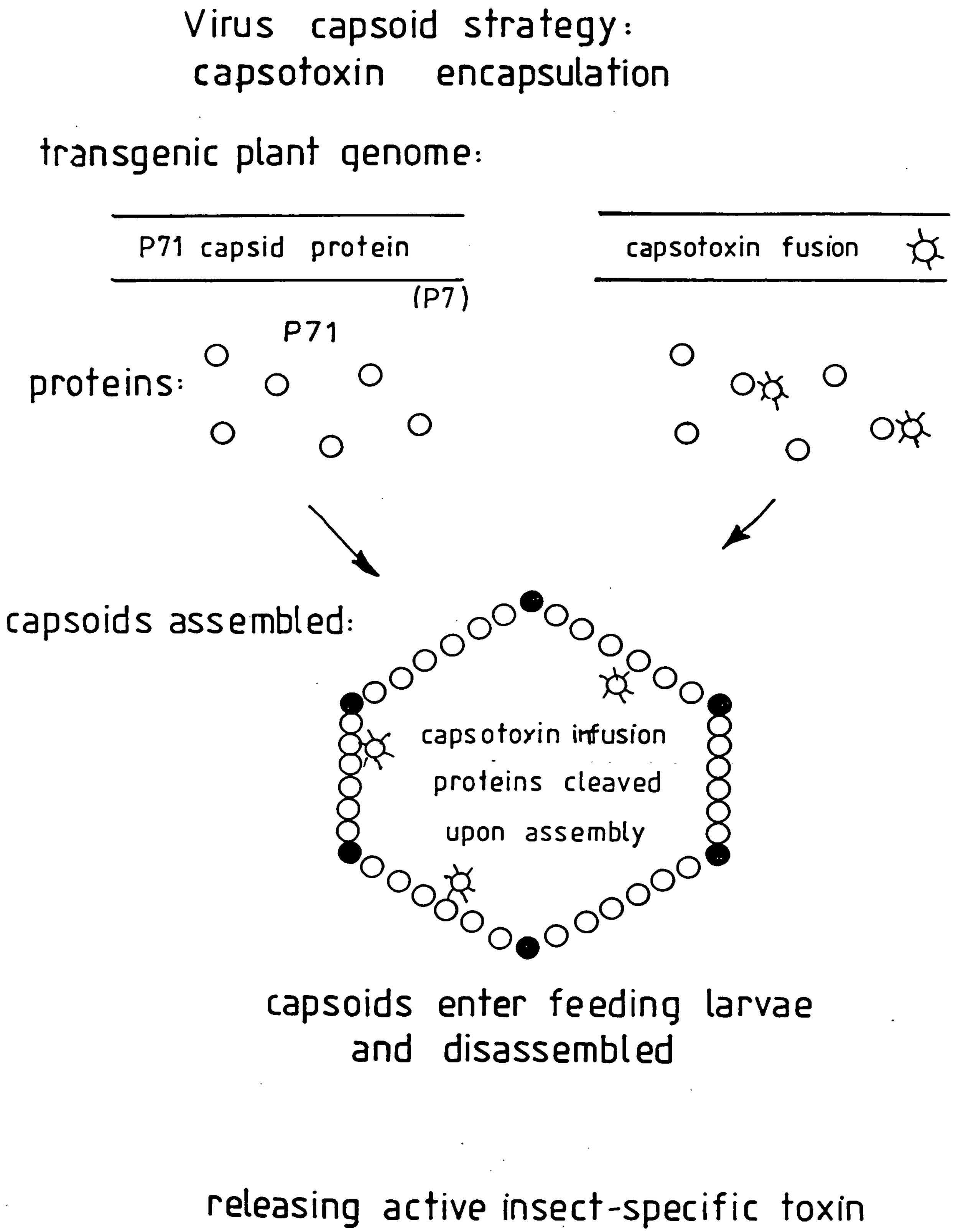

Virus capsoid strategy:
capsotoxin encapsulation
transgenic plant genome:
P71 capsid protein
(P7)
capsotoxin fusion
P71
proteins:
capsoids assembled:
capsotoxin infusion
proteins cleaved
upon assembly
capsoids enter feeding larvae
and disassembled
releasing active insect-specific toxin

FIG. 14a

Virus capsoid strategy:

toxin message encapsulation and amplification

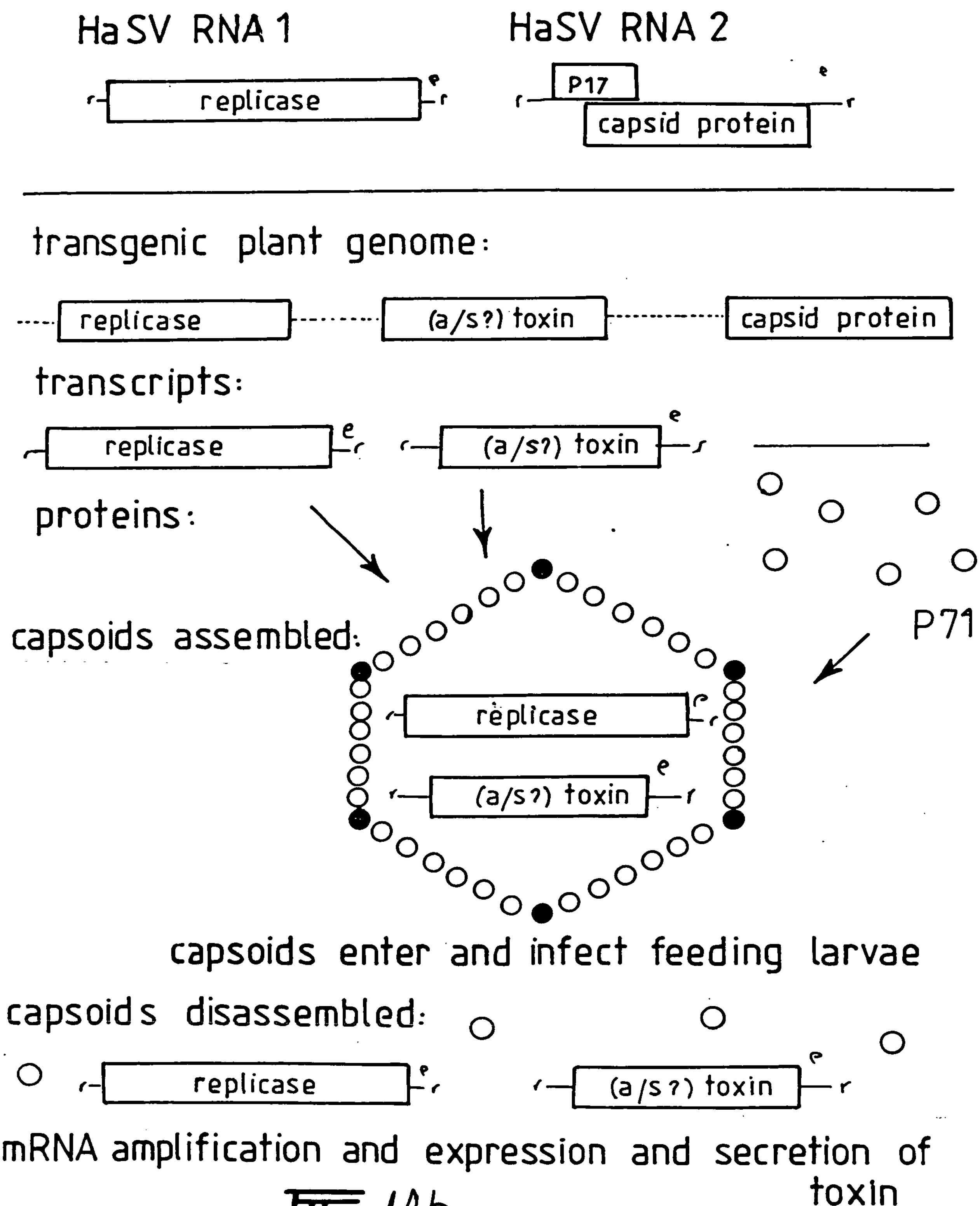


Fig. 14b

Virus expression in plants: the one-way vector

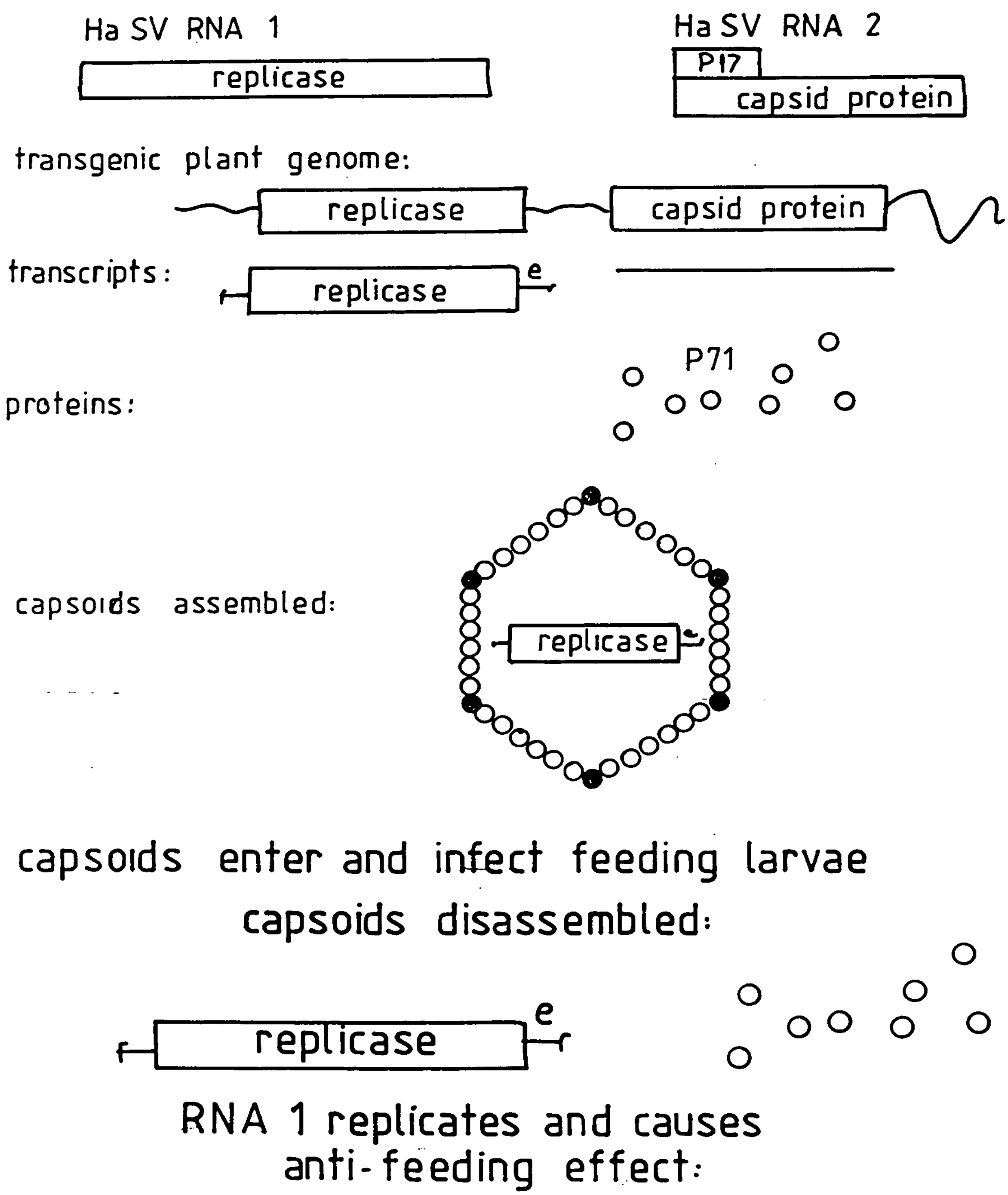


FIG. 14C

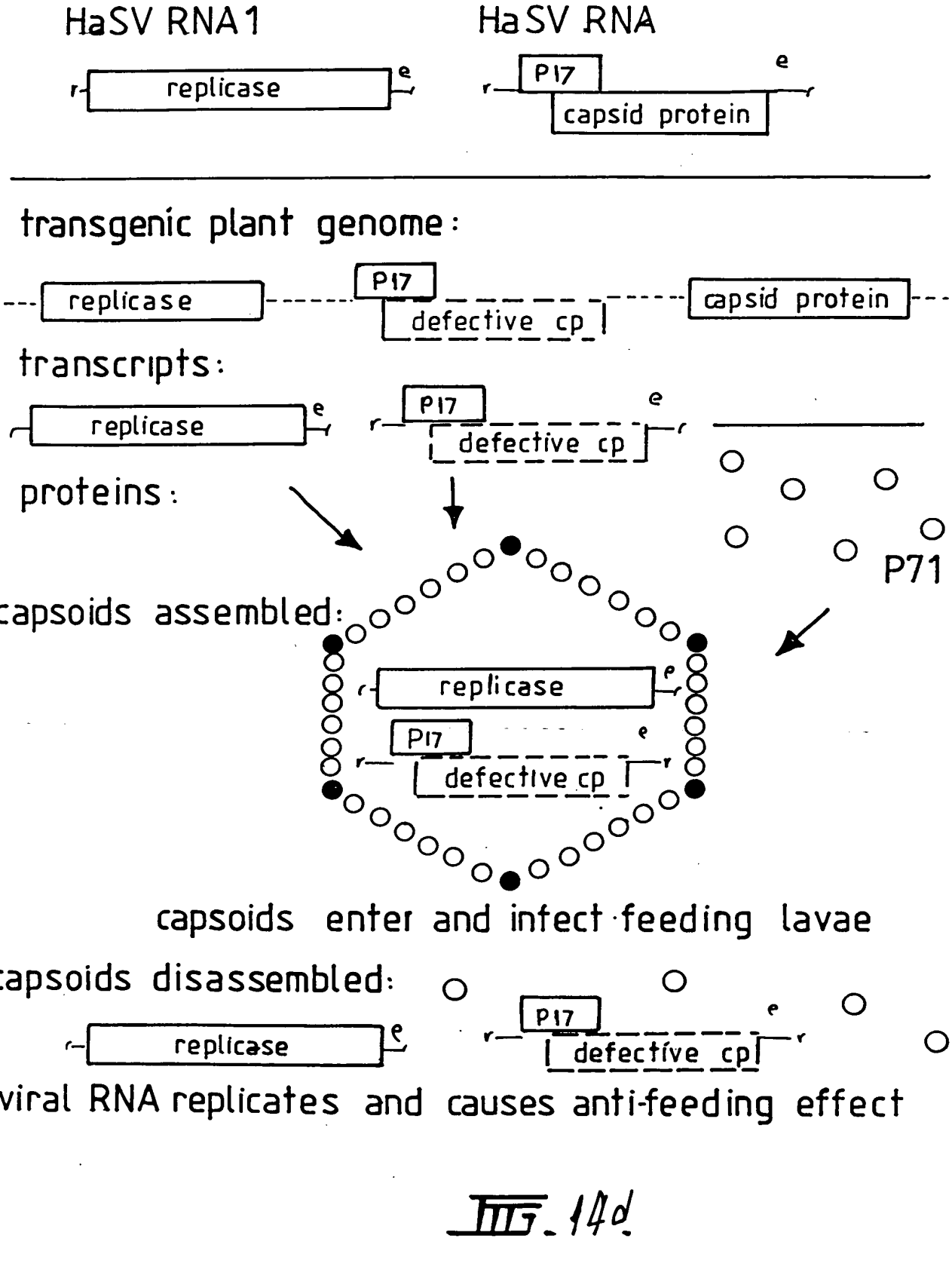

HaSV RNA1
replicase
HaSV RNA
P17
capsid protein
transgenic plant genome:
replicase
P17
defective cp
capsid protein
transcripts:
replicase
P17
defective cp
proteins:
P71
capsoids assembled:
replicase
P17
defective cp
capsoids enter and infect feeding lavae
capsoids disassembled:
replicase
P17
defective cp
viral RNA replicates and causes anti-feeding effect

FIG. 14d

Virus expression in plants

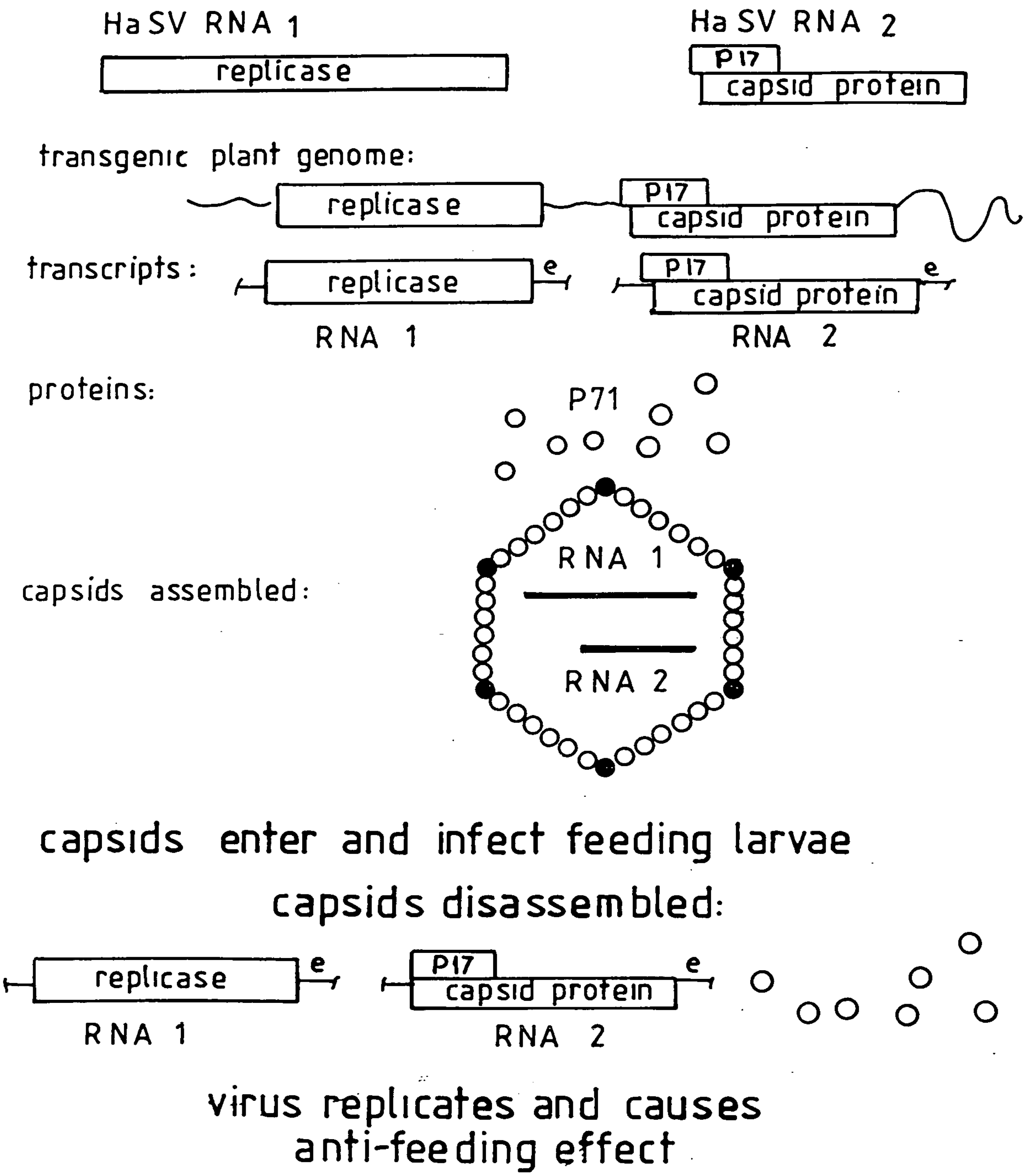
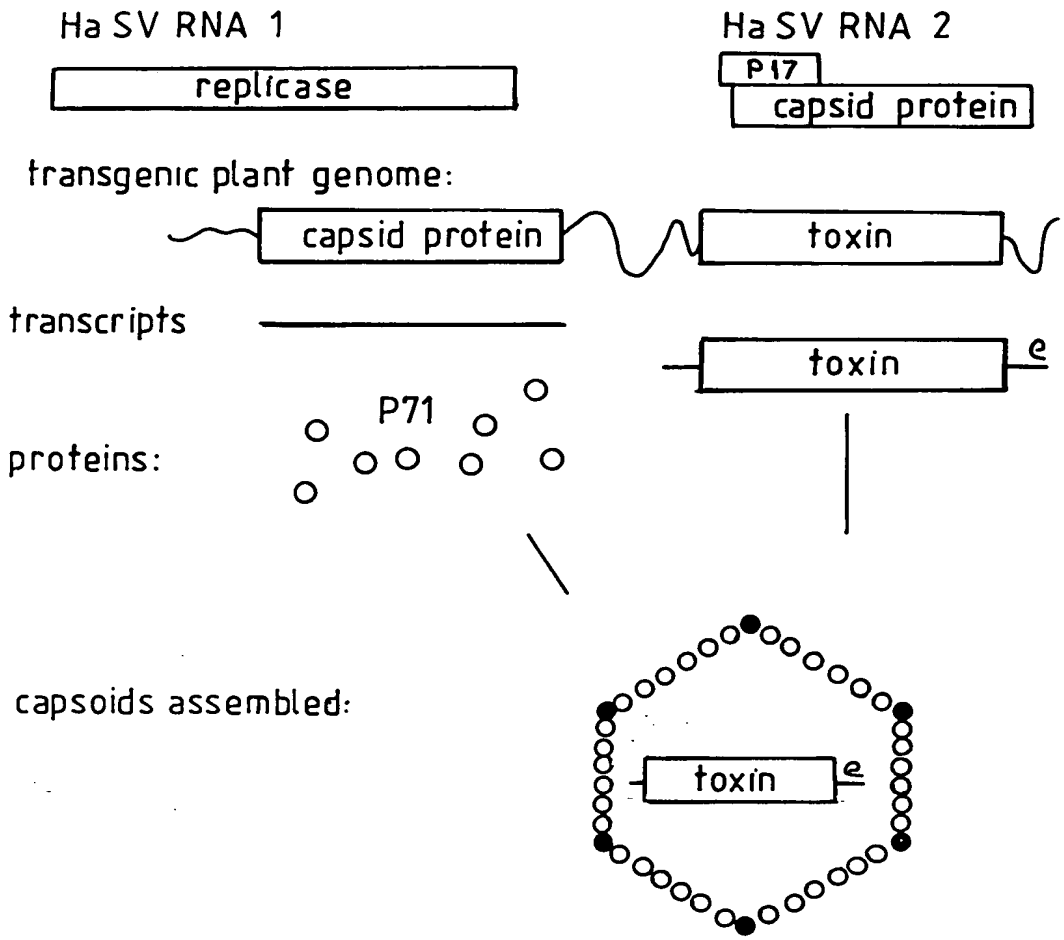


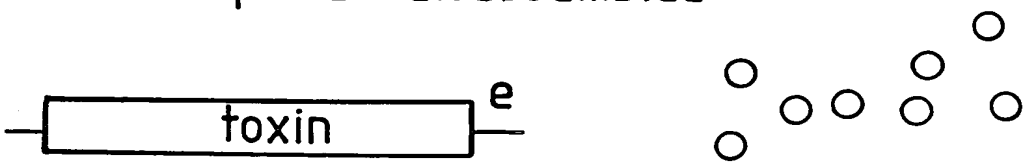
FIG_14e

Virus expression in plants: the one-way vector for a toxin



capsoids enter and infect feeding lavae

capsoids disassembled:



toxin expressed and causes lavae to cease feeding

FIG. 14f

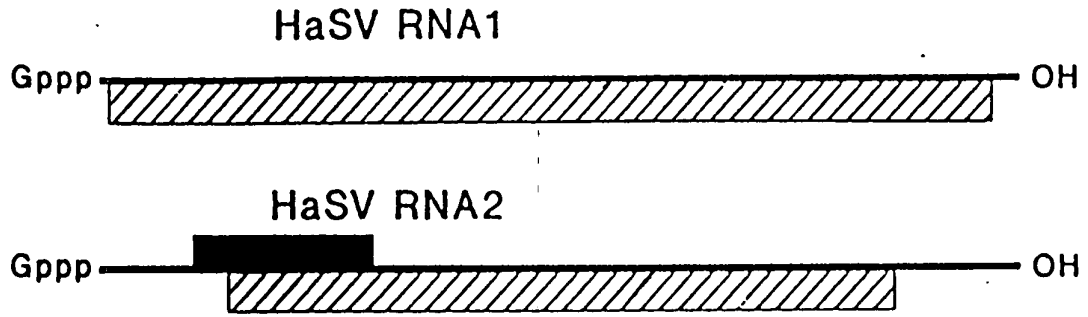


FIG. 15.

baculovirus expression constructs

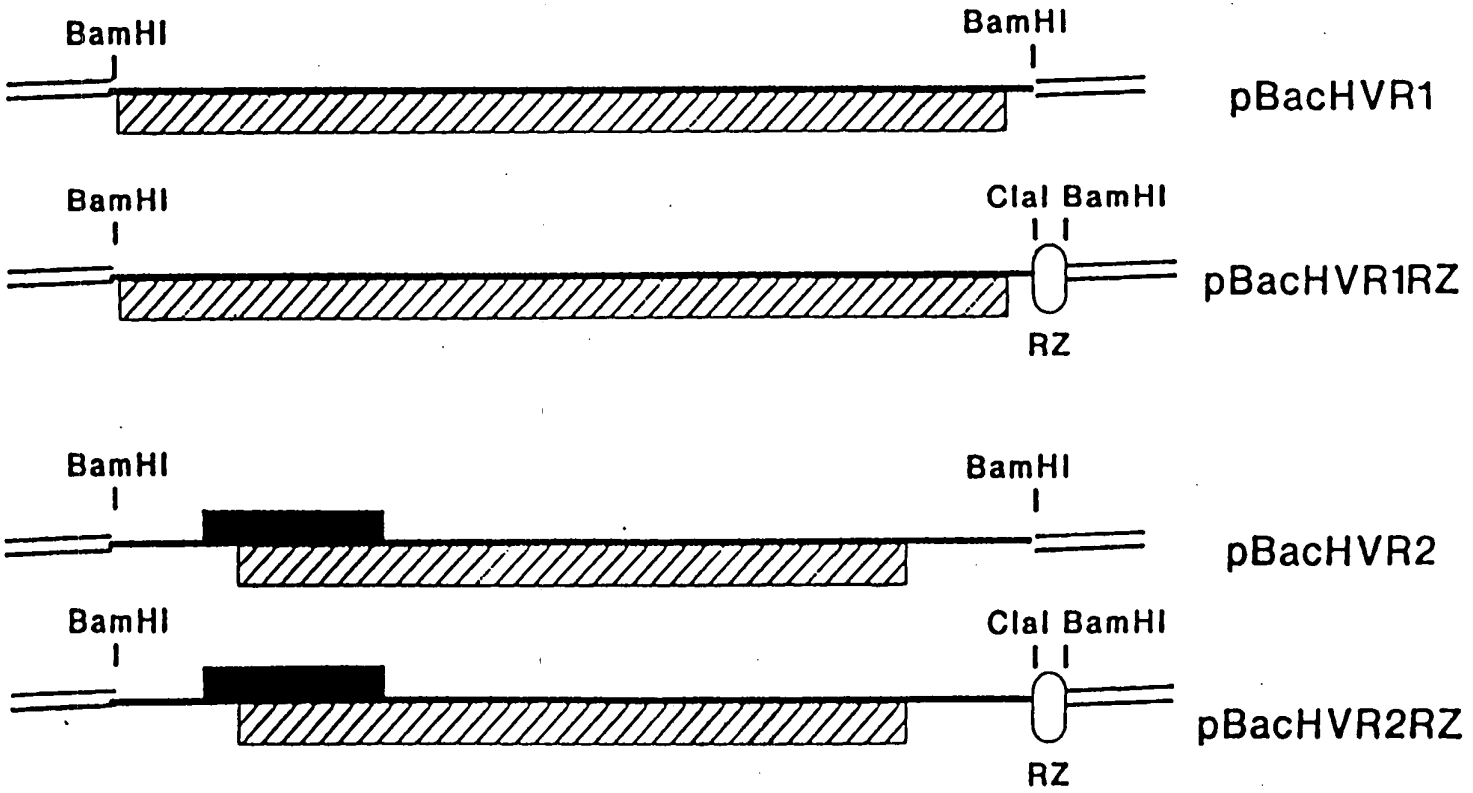
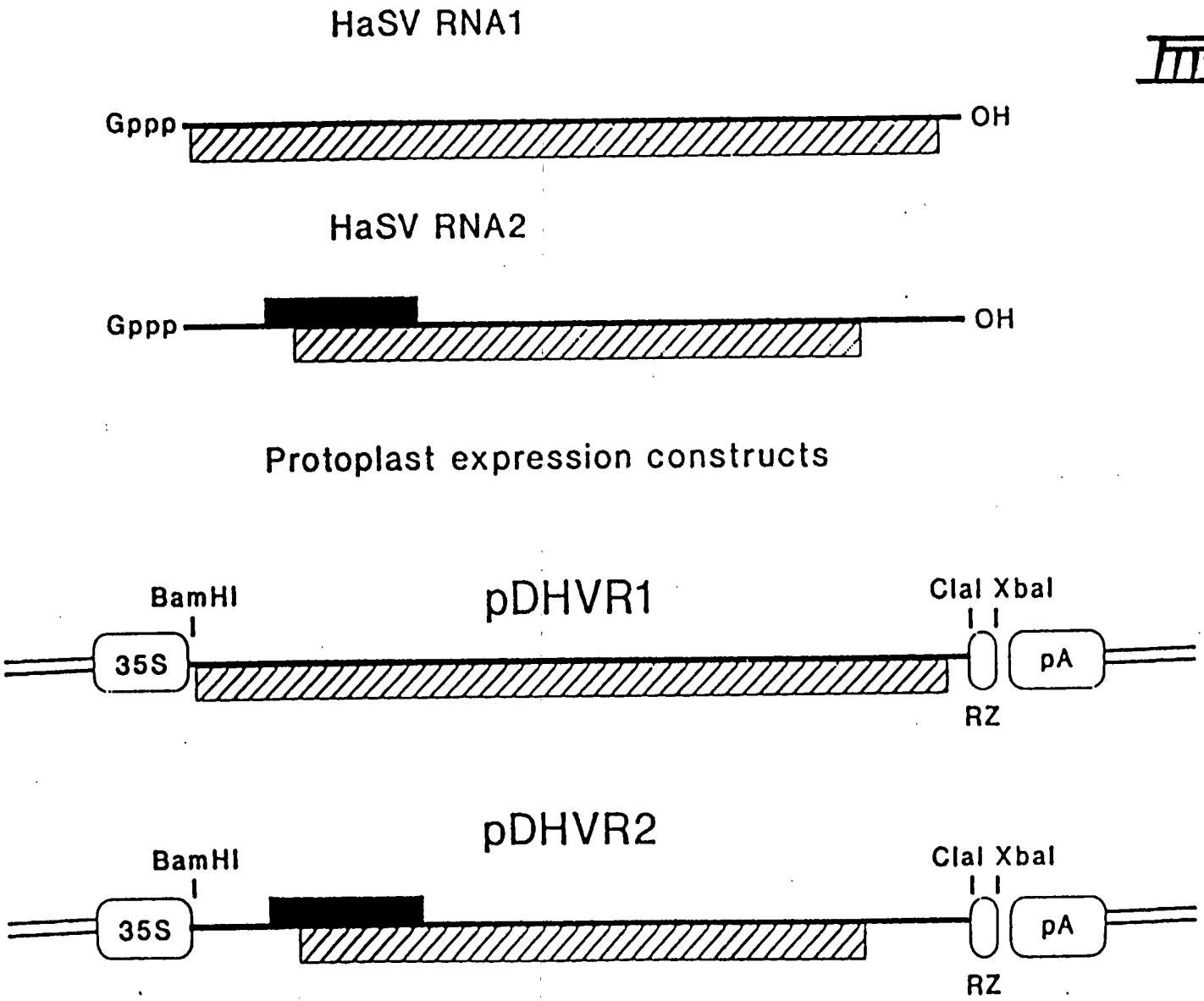


FIG. 16.


HaSV RNA1
Gppp
OH
HaSV RNA2
Gppp
OH
Protoplast expression constructs
BamHI
pDHVR1
ClaI XbaI
35S
pA
RZ
pDHVR2
BamHI
ClaI XbaI
35S
pA
RZ